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<b>(21) International Application Number:</b> PCT/US97/20313 <b>(22) International Filing Date:</b> 5 November 1997 (05.11.97)  <b>(30) Priority Data:</b> 60/030,455                      6 November 1996 (06.11.96)                      US  <b>(71) Applicant (for all designated States except US):</b> WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Mass- achusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA).  <b>(74) Agents:</b> GRANAHAN, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).		<b>(81) Designated States:</b> JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
<b>(54) Title:</b> BIALLELIC MARKERS  <b>(57) Abstract</b>  The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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## BIALLELIC MARKERS

## RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996,  
5 the entire teachings of which are incorporated herein by reference.

## BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution,  
10 generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and  
15 is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In  
20 many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism  
25 (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include  $\beta$ -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater



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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a

5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays

10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for

15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to

20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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## SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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## DETAILED DESCRIPTION OF THE INVENTION

## DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).
- As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with

15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same

20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site

25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include

30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

#### I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference  
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being  
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table  
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the  
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are  
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

## II. Analysis of Polymorphisms

### A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid  
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For  
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.  
10  
15

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),  
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification  
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

#### 30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,



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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

#### 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

## 2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

### 3. Allele-Specific Primers

5       An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in  
10       conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows  
15       a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of  
20       the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

### 4. Direct-Sequencing

      The direct analysis of the sequence of polymorphisms of  
25       the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,  
30       1988)).

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## 5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

## 10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

## 25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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## A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See  
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in  
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with ~ polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population  
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic  
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of  
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime  
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$  is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies  $x$  and  $y$ , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote:  $p(AA) = x^2$   
 Homozygote:  $p(BB) = y^2 = (1-x)^2$   
 Single Heterozygote:  $p(AB) = p(BA) = xy = x(1-x)$   
 Both Heterozygotes:  $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity  $p(ID)$  for a 3-allele system where the alleles have the frequencies in the population of  $x$ ,  $y$  and  $z$ , respectively, is equal to the sum of the squares of the genotype frequencies:

25 
$$p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of  $n$  alleles, the appropriate binomial expansion is used to calculate  $p(ID)$  and  $p(exc)$ .

The cumulative probability of identity ( $\text{cum } p(ID)$ ) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30 
$$\text{cum } p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

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The cumulative probability of non-identity for  $n$  loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5        If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10        B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15        Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20        If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child  
25        attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30        The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A  
5 and B of a biallelic polymorphic site.

(At a triallelic site  $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$ ), where x, y and z are the  
respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

10  $p(\text{non-exc}) = 1 - p(\text{exc})$

The cumulative probability of non-exclusion  
(representing the value obtained when n loci are used) is  
thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots$$

15  $p(\text{non-excn})$

The cumulative probability of exclusion for n loci  
(representing the probability that a random male will be  
excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

20 If several polymorphic loci are included in the  
analysis, the cumulative probability of exclusion of a  
random male is very high. This probability can be taken  
into account in assessing the liability of a putative  
father whose polymorphic marker set matches the child's  
25 polymorphic marker set attributable to his/her father.

### C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to  
the phenotype of an organism in different ways. Some  
polymorphisms occur within a protein coding sequence and  
30 contribute to phenotype by affecting protein structure.  
The effect may be neutral, beneficial or detrimental, or  
both beneficial and detrimental, depending on the



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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of  
5 individuals who have been tested for the presence or  
absence of a phenotypic trait of interest and for  
polymorphic markers sets. To perform such analysis, the  
presence or absence of a set of polymorphisms (i.e. a  
polymorphic set) is determined for a set of the  
10 individuals, some of whom exhibit a particular trait, and  
some of which exhibit lack of the trait. The alleles of  
each polymorphism of the set are then reviewed to determine  
whether the presence or absence of a particular allele is  
associated with the trait of interest. Correlation can be  
15 performed by standard statistical methods such as a  $\chi^2$ -  
squared test and statistically significant correlations  
between polymorphic form(s) and phenotypic characteristics  
are noted. For example, it might be found that the  
presence of allele A1 at polymorphism A correlates with  
20 heart disease. As a further example, it might be found  
that the combined presence of allele A1 at polymorphism A  
and allele B1 at polymorphism B correlates with increased  
milk production of a farm animal.

Such correlations can be exploited in several ways. In  
25 the case of a strong correlation between a set of one or  
more polymorphic forms and a disease for which treatment is  
available, detection of the polymorphic form set in a human  
or animal patient may justify immediate administration of  
treatment, or at least the institution of regular  
30 monitoring of the patient. Detection of a polymorphic form  
correlated with serious disease in a couple contemplating a  
family may also be valuable to the couple in their  
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where  $Y_{ijkpn}$  is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record;  $\mu$  is an overall mean;  $YS_i$  is the effect common to all cows calving in year-season;  $X_k$  is the effect common to cows in either the high or average selection line;  $\beta_1$  to  $\beta_{17}$  are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms;  $PE_n$  is permanent environmental effect common to all records of cow  $n$ ;  $a_n$  is effect of animal  $n$  and is composed of the additive genetic contribution of sire and dam breeding values and a  
5 Mendelian sampling effect; and  $e_p$  is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next  
10 generation of the herd.

#### D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present  
15 section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such  
20 analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84,  
25 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6  
30 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the  
10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction  $\theta$ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &  
15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions ( $\theta$ ),  
20 ranging from  $\theta = 0.0$  (coincident loci) to  $\theta = 0.50$  (unlinked). Thus, the likelihood at a given value of  $\theta$  is: probability of data if loci linked at  $\theta$  to probability of data if loci unlinked. The computed likelihoods are usually expressed as the  $\log_{10}$  of this ratio (i.e., a lod  
25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod  
30 scores for differing values of  $\theta$  (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of  $\theta$  at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of  $\theta$ ) than the possibility that the two loci are unlinked. By convention, a combined lod score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

#### IV. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component) except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or  
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate  
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host  
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include  
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as  
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing  
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, 5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is 10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene 15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating 20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate



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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and  
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to  
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide-fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*  
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of  
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

#### V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific  
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means  
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15

## EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to  
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference  
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and  
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
WI-7070	226	C	T	---	---	TGTGAAACTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACATGCCAGTTGGGAAGGCTCT GAAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAGAGAGAGATTGAGACCAATCTTTATTT GTACTGGCCAAATACTGAATAACAGTTGAAGGAAAGACATTGGAAAAAGCTTTTGAGGATAATGT TACTAGACTTTATGCCATGGTCTTTTC/TJAGTTTAATGCTGTCTCTGTCAG
WI-10744	61	G	C	---	---	AAGCCATTGACGTACATCTCAGAGGTTATTTGCATGGATTGACTCTCTGGGACAAAAGGAC[G/C]AA AAACACTCTTCTGTGGATATCTGTCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTTT GATAATACATAAGCCCCCTAGGATTTAGATACAATCTTGAAGAAACTGAGACAGATAATCTCTGAATT AAATGAGGTAAGTTTCAGGCACCTCA
WI-9975	126	C	T	---	---	GGGCAAAATACCAGCAAAAAGTCAAAATACCAGCATCAAAAGTCAGGTGCAAGGGAGGTAGAACA TTACAGTAACATATGTCAAATCTTTTGTATATAGTATTATCTGCCAATGCCCTAGATA[C/T]JAGTG GGTCCCTAATAGTTATTAGTTCCTTTTCTCCCTCTCTCAITCTCTGAAATTTATTTTATACTTAA GGGATTAGTTACCACCAAAAATGTATGATCAATTTGATCTTACTGAA
WI-8010	247	G	T	---	---	GCTAGGTTTGTTCTGTTGGCTGCTTCACGTAGACTTTGAGATGACTTGATTACAGTAATCCCTATGT GATGTAACGTAGCTAGACCTTCCCTTCTCCGCAATCCAGCTCCAGGTTTCAGAAAGTATGCCACAC TCAACCTTCTCTCCAGTTCACTCCTGTATTAAATTTCTCCCATATTAATTCAAAGGGAGTGGACAGGT CCCTGGCTGAAAAGAAATAAGAGATCCCAAGTGGTGGGG[G/T]CTT
WI-5222b	85	G	C	---	---	GCCGGCCTATCTTTAAATTTAACTTGATCTTTGGGTCTCTCCATCCTAGGATTCGCCTTATAAT CTTTGTCTGTCTGTA[G/C]JATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGGCCAATCTCAGGTCTCTTGAATTTTCTGCTATTGAGGACATTTCCACTTTCTACTTAA TCTGACTCTATAACAACCTCCACAGAA
WI-5222	52	G	C	---	---	GCCGGCCTATCTTTAAATTTAACTTGATCTTTGGGTCTCTCCATCCTA[G/C]GATTCTGCCTTAT AATCTTTGCTCTGTCTGATGATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGGCCAATCTCAGGTCTCTTGAATTTTCTGCTATTGAGGACATTTCCACTTTCTACTTAA TCTGACTCTATAACAACCTCCACAGAA
WI-8007	242	C	A	---	---	TATGCATCTCCACAAAAGCGATATAATTTAAAGTTTTTTTCATTAGAAAATAAATGTATAAAAATAA ATATGTTATTATAGGCATTTATTACTAATAGTCTCTTGGAAAGAACACCCCAACCAATACTT ATAAGTACATGTAAATTTATAGTAACATATTTACTATACATATGGAATAATCATATCTCACA GAAGAGCTGAACAGACATTCACCAGGATACGACTGTGGAC[C/A]JAGCTGCTG
WI-9823	97	C	T	---	---	TCAGTTGCAAAAATGCTGCCATAAAACATGCTTTGCTTATCTCTGTGCATATGATGTGTTTTGTTAG TCTATATTCACACATAGAGTGAAATTT[C/T]GGGGCATGGGAAATACATCTTTATGAGACATTTGA ACTGCTCACCACATCATAGTATCCATTTAAACAGACCAACATGTATAAGAAATCCCTTTGTTTTAG ATGCTTCCCAATCTGATTTGATGACTATTGATGCACAGTTGGATCACC

WI-9651b	105 A T ---	---	TCTCTACATTCTATGGACAACCTCCATGCCCTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTCCT ACTTGTCCCTCATGTACAAATTTCTGCTGTCTCTCA/JTGGGGCAGCTTGCAGGCCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGACACTGCCAGGGACCCCTATAGGCCCTCTG TCTTAAACCTGTAAATGGTATATTAATCCTTGGTGTGAATGCTCTC
WI-9651	139 T C ---	---	TCTCTACATTCTATGGACAACCTCCATGCCCTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTCCT ACTTGTCCCTCATGTACAAATTTCTGCTGTCTCTCAAGGGGCAGCTTGCAGGCCCTCCCTTTAGACACCT CT/JACAGGTACAGCCGACCATGCCCTACCTCCATGCCACTGCCAGGGACCCCTATAGGCCCTCTGT CTTAAACCTGTAAATGGTATATTAATCCTTGGTGTGAATGCTCTC
WI-7676b	309 A C ---	---	GTGACCTTCTGTCAGCGTGGAGATGGACATCCTTGTCTGGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCGGCTTCTCTGGTGGCTGTGGTTCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGTGTGTGC TCCCCCGTCTCTGAGGCGAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	GTGACCTTCTGTCAGCGTGGAGATGGACATCCTTGTCTGGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCGTGGCTTCTCTGGTGGCTGTGGTTCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGTGTGC GTGCTCCCCCGTCTCTGAGGCGAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	CATTATCTGTCTGGGTCTGTTTCATTCACCTTCTCTCTCCAAATGAAGAGATATTTAAGCATCAT CATCTGGCCCTTTTGTGATTTGAATATTTTGTG/JAGTCACTCCTATGCACATGATAAATTTGTTA TGCTGTCTTATCTTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAGGGA TCACCCCTTTTGGCTCTACAACCTTATAGATATTTAAATATCTTTT
WI-9986	42 T C ---	---	TTGGTGTGAACCTCAGAAATATAGGAAATAAGACAAATTTGAAT/A,CJGTACCCCGAGGAACAAGAG CCCTGCACCTTGACTCCAAAGGAGTCTATTTATCTGGCTGTTCCAGACTTTATTTGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTCACAAGAACATGTCA ATATCAATAGCATGCATATGGGTGTGGATTCTTAGAACTTATTGCAATT
WI-7041	174 C A ---	---	GTCTATTGCAGGAGAAACGTCCCTTGGCACTCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGCCCTGCACATGCAAACTCCAGTCCCTGCCTTCAGAGAGCTGAAAAGGGTCCCTGGGTCTTTTATTT CAGGGCTTGCATGGCTCTATCCCCCTCTGCCCTCTC/JCCACCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGAACAAGCTCATTTGTACAGTGTCTGTATGTAATAA
WI-7224	134 T C ---	---	ATAAACCTTGTGTATGTATCACCCCAACTCACTAATATCACTATGTGCTATCAGATATCCTCTCT ACCTCAGCTTATTTGAAGAAAATCCTAAACATCAAACTATTCATCCATAAAAATGTGAGCATTT /CJATTAAAAACAATAACTTTTAAAGAAAACATAAGGACACATTTTCAAAATTAATAAAAAATAAG GCATTTAAGGATGGCCCTGTGATTATCTTGGGAAGCAGAGTGATTATCATGCTAG

WI-10826	132	A C ---	---	TCTATTGCAATTCACAGTAGCCCCCATGAAGTAGGTATACCGCCTCTATTTAAACATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTCTTAATAGCAAGACCTGCAIAC JCCCTGGCTTCTGACTCCAAAGCTTATCCCTTCTCATGCTGTGCTGTAGCCAGGACCCCATGCGCA GAAAGCCAGCCTCTCCATCCCCAC
TIGR- A004S25	145	G A ---	---	AGATCTGCCATTAGTATTATTCCTTTGAAGATACITTTGGAGATTCATTTCTTGAGTGGCACTGCAT GCTCATTAGTGAAGAACTTTGGGGTATAGAAATGGAATGGAGAGTTTCAAACAGCTTTGCTGAAAC TGACTTTGG[G/A]CTCCAGACTTCACTGTCTTAGGCAATTGAACCATCACCTGGTTTGCACTTCTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24	A T ---	---	AAACACAGAAATCATCAAAGCACIATATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAGTAACTCTGAATAGTAGGATAGTATTATCATTTCTGTATAGATTCACCTCTCAGCAAT TGGTCTGTTTCACTTATGGAACCTCTCGTACTGTAAATTTTCACTTATGGAACCTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121	G T ---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATAGAACACTTTGAATGGTCTTGTC TTTCAATAAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCACCTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAGAAACCTTGAT
WI-4719b	107	T G ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTTAGGGCTAGTGTCTTTGGGTGTAGCGGATT ATGCTGACGCCATGGGTGTTCAATAGTGACTTGAGAGTT[G/A]CTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACTTGCAACTTATCCTTAAGACATTTTCACAGGA
WI-4719	70	G A ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTTAGGGCTAGTGTCTTTGGGTGTAGCGGATT AT[G/A]TCTGACGCCATGGGTGTTCAATAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACTTGCAACTTATCCTTAAGACATTTTCACAGGA
WI-9484b	216	G C ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCCAGCAAGATTCTACCTCTTACCCGTGAGG AATACTGAGTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTCTGGAGAGGGAGGGCCAGAGAGGGAATTCAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGGACCAAGGTTCCAAACTTT
WI-9484	178	G A ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCCAGCAAGATTCTACCTCTTACCCGTGAGG AATACTGAGTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTCTGGAGAGGGAGGGCCAGAGAGG[G/A]AGGAATTCAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCAAGGTTCCAAACTTT





WI-931c	191 C A ---	---	GACCAGGGCACCAGAAAGCCACGGAGCCACAGCCACTAGCCCTGAACCTTGAACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCATTATCTGCTGTGTCAAAATGATCCTCT GTTGCTGCACTGTCATTACTGTTGATGGATTATAATTATTGTCCTCAAAAAGCC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTA/GJTCCCTCACCACACCTTCCAGTGCATTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCATTACTGTTGATGGATTATAATTATTGTCCTCAAAAAGCCCTGGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAGCCAC/A/GJCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCATTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCATTACTGTTGATGGATTATAATTATTGTCCTCAAAAAGCCCTGGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91 C T ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCAITTTAAACGTTGCCCCCCC
WI-10870	103 G A ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGACCTACTTAGA[G/A]CAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCAITTTAAACGTTGCCCCCCC
WI-7719b	281 T C ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCCTCCTACTGATGATTTCAAGCTAAAGCAA
WI-7719	163 A G ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[C/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTCTGGACATTGCCCATGTATAATCCTCCTACTGATGATTTCAAGCTAAA
WI-10396	72 C A ---	---	GCCTTGGAGTATATCTAAACTGTGGCCCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA GAGT[C/A]GTGACTTTATGCCCAGTTTCCCTCTCAGATTTTATGACGGTTGTTTCTTTTGTGA TGCCATTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCCATTGCTGTTCAAGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94 C G ---	---	---	TCCCTTTATGCAACCAAGAGATATTTATTAAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCGGTGGCACTCATGGAGGGG[C/G]TGCAAGTTGGAACATATGCAAGTGTCTCCGGCCACACA TCCTGCTGGGGCCCTACCCTGCCCAATTCAATCCTGCCAATAAATCCTGCTCTATTGTTTCATCCTG GAGAAITGAAGGAGGTCAAGTTGTTTGCAATGATTGTGAGAGAACCT
WI-7842	57 T C ---	---	---	CACAGCCATGCCCTTGAGGAGCCGCCACCAGATGCTGAATCCCCTATCCCATTCGT[C/G]GTATGAG TCCCATTTGCCCTTGCAATTAGCATTCGTCTCCCCCAAAAGAAATGCTATGAAGCTTTCTTTCCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGCTTAGTACCAGAGCTAGTTTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAGCAATGATTCAGCTCCCTTATA
WI-7721	145 A C ---	---	---	CTGCCATCACGCCACTGGAGTCCACACTTTGAATTTGGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCACATCCCACCCACAGCTGTACCCAGCCGGGAGGTGCGAGCCCTTCCCTCCC TGCTCTGC[A/C]TCTGACTCTCTTTTGAGGTCCCTGTATGCTACCTCTGACTTCTGTGGTCCCTCTG TGCTGCTCTCATCCATTCCTTACTGGGGCCTGGGGCTCTAGCCCCA
WI-4767b	173 C A ---	---	---	TTTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCCT CAGGCTGGGTAACTCTAGATCTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATGTTT CTTGCCCTTGAGAAATCCTAGAAGCACAGGGATGACA[C/A]AAATCACTAAGGAATCCCACTAAGA CTCCTTAACCCAGAGATTTTAACCT
WI-4767	50 A G ---	---	---	TTTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGA[A/G]ATTCATAAAGAGTT CCTCAGGCTGGGTAATCCTAGATCTTCTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATG TTTCTTGCCCTTGAGAAATCCTAGAAGCACAGGGATGACACAAATCACTAAGGAATCCCACTAAGAC TCCTCTAACCCAGAGATTTTAACCT
WI-7718f	222 C T ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAACTATGTATTAAAT
WI-7718e	60 T C ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT[C/G]CAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCCATGCAGGAAGGAAACTATGTATTAAAT
WI-7718d	31 G A ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCCATGCAGGAAGGAAACTATGTATTAAAT

WI-7718c	91 C G ---			---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCGJTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
WI-7718b	248 A G ---			---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGTG ACTTTCAGATGGAAGAGGTGAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTJAGJAT
WI-7718a	42 A T ---	C		---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCJAC, TGTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTA
WI-7227d	99 G C ---			---	AGGGAATTGTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTAGACAAAGCTTTAGJAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---			---	AGGGAATTGTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTTAGTATCTGTGTTCCGGTGGGTGAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACAGTG TTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93 G T ---			---	AGGGAATTGTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---			---	AGGGAATTGTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC TTCCGTGGACCAATTCATCTTTAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---			---	CCACAAATGCTCTCCACGATGTCAGGACTCCTGTCTGCTGGAGGTGGGAGACAAAGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGCTATGTTGTGATCCTTCATCGAACAACTGATCGGAAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACTGAGCCAAACACACTGTAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCAJACJATGATCTTGAGATTTC

WI-7310a	64 T A ---	---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGTCTGGAGGTGGAGACAAGGAACCTTAA JCCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCCTTCATCGAACAAACTGATGCGAA AACTTGAATCTGTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACTGAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	---	CCAGCAACACCTACACCTTTGTCACCTGCCCTGGACTCCTATGATGGCCTGCTGGTTGATAATAATCA GATCATGCCAAGACGGCCTCCTGATAATCGTCTGGGCATGATTGCAATGGAGGGCAAATGCGTCC CTGAGGAGAAAAATCTGGGAGGAGCTG/G/GTGTGATGAAGGTGTATGTTGGAGGGAGCACAGTGT CTGTGGGAGGCCAGGAAGCTGCTACCCAAAGATTGTTGGTGCAGGAAAACTA
WI-7878a	51 C G ---	---	---	CCAGCAACACCTACACCTTTGTCACCTGCCCTGGACTCCTATGATGGCCTG/G/GTGGTTGATAATAA TCAGATCATGCCAAGACGGCCTCCTGATAATCGTCTGGGCATGATTGCAATGGAGGGCAAATGCG GTCCCTGAGGAGAAAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGAGGGAGCACAGTG TCTGTGGGAGGCCAGGAAGCTGCTACCCAAAGATTGTTGGTGCAGGAAAACTA
WI-7381c	213 C T ---	---	---	CTCCACATCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTCTTTCTACCC AGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCCTATGGTGAGATC AGATGTGGCCAAAGGAAGGAGCTCTGTTTCCAGAGAAATTTGCACAAAGTCCCTCTGTACAGAGACA AAACGGCCTC/G/GTGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	---	CTCCACATCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTC/G/GCTTTCTTCT ACCAGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCCTATGGTGAG ATCAGATGTGGCCAAAGGAAGGAGCTCTGTTTCCAGAGAAATTTGCACAAAGTCCCTCTGTACAGAG ACAAAAGGCCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	---	CTCCACATCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTC/G/GCTTTCTTCT ACCAGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCCTATGGTGAG ATCAGATGTGGCCAAAGGAAGGAGCTCTGTTTCCAGAGAAATTTGCACAAAGTCCCTCTGTACAGAG ACAAAAGGCCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	---	AAATTGCTCTATTCCGACCCTCATATTAAATAAGAGCAATGAGAGCGGGAATAATTGAACCTCTCTC AGGTACTGACTGTGGACCAGACAAG/G/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTCTTCCCATTTACAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTCAAATAAGGAGTGTGTGAGGTTTGTGCC
WI-1017a	92 G A ---	---	---	AAATTGCTCTATTCCGACCCTCATATTAAATAAGAGCAATGAGAGCGGGAATAATTGAACCTCTCTC AGGTACTGACTGTGGACCAGACAAG/G/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTCTTCCCATTTACAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTCAAATAAGGAGTGTGTGAGGTTTGTGCC



WI-1126a	97	T C	---			CTCTATTCTCTGGGCACTGCTTCTTTGGGGGCAAACTCCAGTATCACTGATACATAATAAAAA CCCTGTAGTCTGCTTGCATTTTCAAGATTC/CAATATATATCCAGATGTTTTTCCAGCAAGAAA ATTTTATTTCTCAAGATATAAAAAATAATATTTAAATTCAGTTTCCCTCAAAAGGAATATGAAATTT GTTAAATGCAAAATCCAGCTGTAACCTTTTGGACTTGCTTTTATTTCTT
WI-11183c	124	C T	---			TAGTGCTAATTTTGGAAAGTTTGCTGATTTTAAAAATCTTTTAAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATCAGATGATTTTGGCCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTTTAAATATTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192	T C	---			TAGTGCTAATTTTGGAAAGTTTGCTGATTTTAAAAATCTTTTAAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATCAGATGATTTTGGCCCTTGTCACATAACATTT ATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTTTAAATATTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118	C T	---			TAGTGCTAATTTTGGAAAGTTTGCTGATTTTAAAAATCTTTTAAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATCAGATGATTTTGGCCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTTTAAATATTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174	G A	---			GCTTGGTTGCTTTAGTCTTATTGCTCAGTCTGAGTTCTCCCTTCTGCTGCGCCCTTTTGTATTCA CCCATACCTCTATGCCCTGCTCAGACCATTTCTCTATCTGGAGCGCTCTCCCTTGACTTTCTCTG TTCACCAACCTTCTTTTATCTTCAGGACACTCA/GAJTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTTTCCC
WI-10770a	49	G T	---			GCTTGGTTGCTTTAGTCTTATTGCTCAGTCTGAGTTCTCCCTTCTG/CTCCCTGGCCCTTTTGTATT TCACCCATACCTCTATGCCCTGCTCAGACCATTTCTCTATCTGGAGCGCTCTCCCTTGACTTTCTC CTGTTACCAACCTTCTTTTATCTTCAGGACACTCAGTTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTTTCCC
WI-9667b	82	C T	---			GATGACAACTTCTGCTGTGACCCCTTAGTCTCTGCTCATGACACTTTTCAATCTCTGCTGTATCATGG TTATCACTGGACA/C/JAGCCACCTCCCCAGCAGGCTTAGAACTCCATGAGTAAGGAGCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT
WI-9667a	68	G C	---			GATGACAACTTCTGCTGTGACCCCTTAGTCTCTGCTCATGACACTTTTCAATCTCTGCTGTATCATGI G/CJTATCACTGGACACAGCCACCTCCOCAGCAGGCTTAGAACTCCATGAGTAAGGAGCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT

WI-10400d	189 A G ---			ACATTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAGCACCTTACTAACACAATATTTTATTCTAAATTT TCCTCCCTTACCTTACTCTCCACCCCAAAATAACGTAAGTACCTATGTC[A/G]TGCCATGTAG TTTTTGGTTCATTACTTGCAAAATTATTCAAAGGCGTTAATGCATTATG
WI-10400c	166 A C ---			ACATTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAGCACCTTACTAACACAATATTTTATTCTAAATTT TCCTCCCTTACCTTACTCTCCACCCCA[A/G]AAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTACTTGCAAAATTATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---			ACATTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAGCACCTTACTAACACAATATTTTATTCTAAATTT TCCTCCCTTACCTTACTCTCCACCCCA[A/G]AAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTACTTGCAAAATTATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---			ACATTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTAGCACACATGTAGCACCTTACTAACACAATATTTTATTCTA ATTTTCTTCCCTTACCTTACTCTCCACCCCAAAATAACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCATTACTTGCAAAATTATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---			AAAGGGCTACAACTAAGGCCAAAAACCATGAACGGTATAAGGAGGGTAATGCAAGGGGAGACCC CACCTCTACCA[C/T]TAGAAAAGGGCATTTCAGCACATTCATGAGGCTTCATATCTGTTAG CAACAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---			AAAGGGCTACAACTAAGGCCAAAAACCATGA[C/T]GGTATAAGGAGGGTAATGCAAGGGGAGA CCCCACCTCTACCACTTAGAAAAGGGCATTTCAGCACATTCATGAGGCTTCATATCTGTTAGC AAACAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATACTGAGATGCTGGGCTGTCTCCCTTCCAGGATGCTGGCCCCCAGCCTGGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTGAT CATTTTATATGAATAAAAGATCCTGCAATTTATGGTGTAGTCTGAGTCC
WI-7038b	140 A C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATACTGAGATGCTGGGCTGTCTCCCTTCCAGGATGCTGGCCCCCAGCCTGGCCAGAC AAGA[A/C]GACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCAATTTATGGTGTAGTCTGTA



WI-7038a	31 G A ---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAAATAC TGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCA GACAAAGAGACTGTCAGGAAGGTCGGAGTCTGTAAACAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCGCAATTATGGTGTAGTTCTGA
WI-3429b	64 G T ---	---	ATACGCTTCTGTCTGTCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCCACACAG[G/T] CCCTCAGCCCCCTCAGCTTTGCATGTGTCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCAGTCTCTCTCTGGATTGGATCTAGCAAGACAGACGGTCTCTAGAA TCCTGACTGTTAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-3429a	62 C T ---	---	ATACGCTTCTGTCTGTCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCCACAC[G/T]AG CCCTCAGCCCCCTCAGCTTTGCATGTGTCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCAGTCTCTCTCTGGATTGGATCTAGCAAGACAGACGGTCTCTAGAA TCCTGACTGTTAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-6786c	151 G A ---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAGTGACGGTGACCT GTAGCCCCCATTTCT[G/A]TGGGATAAGGTGCCATTTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786b	111 A T ---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGAT[G/A]AAGAGTGAGTGACGGTGA CCTGTAGCCCCCATTTCTGTGGGATAAGGTGCCATTTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786a	106 A T ---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAA[G/T]GGATAAAGAGTGAGTGACGGTGA CCTGTAGCCCCCATTTCTGTGGGATAAGGTGCCATTTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6711b	226 G T ---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAATTGAATAAGTATTGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTTAACCTTCAGTTCCAACTCACTGAAT TTCATATACCTCCATTATTAAATCAATACATCATTCGAGAGAAAAGACAAACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACAG[G/T]GGCAACTAAGTGTATCTCTAAA
WI-6711a	36 T C ---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAA[G/T]GTAATAAGTATTGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTTAACCTTCAGTTCCAACTCACT GAATTTTCATATACCTCCATTATTAAATCAATACATCATTCGAGAGAAAAGACAAACGGTGCCAACTG GGTTTGGTTGGTGGCTGCACACCCACAGTGGCAACTAAGTGTATCTCTAAA

WI-10613b	172 A C ---	---	---	ATGTATGCCAAAATCATAACCCCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTTGAGCCATA TGGTGAAAAATTTAGAAGTATTATCTCTATATGTATATACAGTTTAAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAAGGCCAGGCAATTTATTGACGCTAGGAGGTTACTATAATTTAGA AAGGCTCTACCTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44 G A ---	---	---	ATTGTATGCCAAAATCATAACCCCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTTGAGCC ATATGGTGAAAAATTTAGAAGTATTATCTCTATATGTATATACAGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTATTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTACCTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133 A T ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCCTTGAAGC ACATCCCGCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA(A/ TGGAAATGAACCACTCCCTGCCATTCCTTATAAGAAATATCCCAAGACCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
WI-7587b	81 G A ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCCTTGAAGC ACATCCCGCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCTTATAAGAAATATCCCAAGACCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
WI-7587a	28 C T ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCCTTGA AGCACAATCCCGCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCTTATAAGAAATATCCCAAGACCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
WI-10681b	103 T A ---	---	---	ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTGACTTACGCAAACTCAATCAGCCAAACC ACAGAAAAGCTAAAGACATCCTTTTAAAAAGCC(T/A)AAGACAGCCATTTTAACTAATTCG TAGTTTATGATTTTCTCAAAATTTCCCAACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAGGAGGTGACGCTCTGTAAAG
WI-10681a	41 A T ---	---	---	ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTGACTTACGCAAACTCAATCAGCCAAACC ACCACAGAAAAGCTAAAGACATCCTTTTAAAAAGCC(T/A)AAGACAGCCATTTTAACTAATTCG TAGTTTATGATTTTCTCAAAATTTCCCAACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAGGAGGTGACGCTCTGTAAAG
WI-7222c	126 G T ---	---	---	GCCTCTCCCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGCTGCTTGAGATGCTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCACCCCTGTTCTCAAGTTGGGGGATGGG(G/T)AATAA AGGAGGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTT

WI-7222b	255	G A ---	---	---	GCCTCTCCTCAACTGTCTGGACCCAGGCTAGGAAAGGGCTGTGAGATGACTGTGGTCCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCAACCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGAATTCCCTTGAACAAGAAGAACTGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGAAGGTGTATTTCAAGAACTCGAATTCATTTCTCA
WI-7222a	126	G T ---	---	---	GCCTCTCCTCAACTGTCTGGACCCAGGCTAGGAAAGGGCTGTGAGATGACTGTGGTCCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCAACCTGTTCTCAAGTTGGGGATGGGIG/TAATAA AGGAGGGGAATTCCCTTGAACAAGAAGAACTGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGGTGTATTTCAAGAACTCGAATTCATTTT
WI-8054d	41	C A ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTCAATATCTCTCCAGTTCAAAATG CTTGATCTTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGGCACCTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTACATAACGCCGCTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-8054c	237	G T ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGGCACCTCAAGCCTTAGCAAA TCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCTTCC TGTACATAACGCCGCTTCCCTGGGCGTACAGAGA/TAATCTCTTGCCCTT
WI-8054b	148	T C ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGGCACCTCAAGCCTTAGCAAA TCTCTTTGTAGT/CJT TAGCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTACATAACGCCGCTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-8054a	131	C G ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGGCACCTCAAGCCTTAG/C/GJA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTACATAACGCCGCTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-10854b	152	G T ---	---	---	TTCCACAAAACCTTCCCTGGCCGGGTGACTAAGATGAGAAGTGGGAGAACTGGATGTTTAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAACACGAAAGCAGATAGTTAACGTCGTGTAAGTTTAT ACGGTGTGCGAGGCAACA/G/TGGAGAGGTACGGGAATAGTTCTACTTCTTGTTTTTATTCTGTG TTTTAGACACAGGGTCTGCTGTGTTG
WI-10854a	102	C T ---	---	---	TTCCACAAAACCTTCCCTGGCCGGGTGACTAAGATGAGAAGTGGGAGAACTGGATGTTTAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAACACGAAAGTAAACGCTGCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTCTACTTCTTGTTTTTATTCTGTG TTTTAGACACAGGGTCTGCTGTGTTG

WI-9826b	127	G A ---			---	AATTTATATGTGAAGGTTAGCAAACATATGCCACAGGGCCCATCTAGCCATGCCATATTTTGTG TGCTGATGGCTGTTGGTGTGTTGCACGAGTTGAGCCATTGTGACAGAGGCTGTTATGAGCCTT CAAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTTGGCTGATTCTAGATATTTAAA GGCAGAGAAGATCAGAAAGTGTGAA
WI-9826	125	A T ---			---	AATTTATATGTGAAGGTTAGCAAACATATGCCACAGGGCCCATCTAGCCATGCCATATTTTGTG TGCTGATGGCTGTTGGTGTGTTGCACGAGTTGAGCCATTGTGACAGAGGCTGTTA/TJGGCCTTC AAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTTGGCTGATTCTAGATATTTAAAG GCAGAGAAGATCAGAAAGTGTGAA
WI-15986	60	T G GTGGGTTTT	TTGTTTGTGT	TGACATTATAT	AAACGTAAAA GAAAATGT	CGGACACGTGATATACAAATACAGATCGTATGGGTTGTTGTGTGGGTTTTTTTTT/GJTTAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A G AG	AACTGCAAAT AGGAACCAG	CCACTGGGGC TCCC	CCACTGGGGC TCCC	TTCAAGTAAGTCAAATAGGAAACCAGAGAG/GJGGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGGAGGAGGTGGCCCCCTACACCCCTTTAT
WI-8170b	259	G A ---			---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACAGAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGAGAGATTACAAAGTTAAGATCATGTGCCATCAAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAGGGCCCTCAAATGAATCTACGGAAAAACATAACACAAGA
WI-8170a	204	T A ---			---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACAGAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGAGAGATTACAAAGTTAAGATCATGTGCCATCAAAGTGCAATCCTATCAATCAGAA AT/AJAAAGGTAAGGGCCCTCAAATGAATCTACGGAAAAACATAACACAC
WI-8172	136	C G GACA	CCTTATTAAA ATTGTTTCTT	GAAGAGAAAT GTAATACCTGT	GAAGAGAAAT GTAATACCTGT	CAGGATTCCTTAAGTCATCTCCAACTACTCCAGGTACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACCTCCCTTTATTAAATTTGTTTTCTTGACAT A/C/GIAGTACCTTTACAGGATTACATTTCTCTCACCGTTTACA
WI-8183	56	G A TGC	TGAAATAAAA ACAAATTTCTGT	TGTGTTGAAAT CAACCTGC	TGTGTTGAAAT CAACCTGC	AGCAGGGTTTGAATTTGATCCCTTATTTTACATGAAATAAAAAACAATTTCTGTGTC/GA/GCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACCAAGCTCGTTTCTGATGCAAGGACAAATATCCCAAT ATTTAAACCTGCAAGCACCATGC
WI-14149	83	CT ---			---	GCTTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAACCCCAAGCATGGGATTTGCCGGAAAT ATTAGCGTTAAAGGAG/C/TTGAGTTGAGTCAACACACCGG
WI-8712	44	G A G	CACAGGGAAG AGGTAGTGGA	CAGGAAGCCTG ACCATCTC	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAACAGCACAGGGAAGAGGTAGTGGAG/GA/GAGATGGTCAGGCTTCCTG TTCCCTAACAGCAGAGAGCCCGCAGCAACCTAGAAAGCGCTCACCTAGCCTCTTAAT

WI-8827	22	C T	TCCCCTGGGAG TCTCCATGCC ACTATGG	GGCATTAGGAT TTTAGTGTTC C	GGTGCCCTGGGAGACTATGG[C]/TAGTGAACACTAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTTCTTTAGTTCCCTTTCTTATCCACCCAGCTCTCT CTCCGGCCTCTAAAGCTCTCTGTAGACTGTCTCTCCATGCCATTCTCIG/A/TJGCCCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACCTGCTTGTCATAAAAGGTCAGCTATGT
WI-8833	51	A T	ATTCCTG	CCTCACACATT ATAGGGCA	ATTTTATAGCCATGTTGGTAAAGTTCAITTTTCAGTACATGGGTAAACACCCAGGCCCTTTCCC[A]/GJT TATATCCAGGTATGCTACAAAGTTCTTTAACTCTTATCAGAAGTTATTATTACTGTTTCCTTAGAGAG GCTACACAGGCTAAATTCACCTAGTTGGTTGTCTAATGTCTCATTATTTATCCTGAAGCTCGTG GAGGGACTTAACCTTTGGCCT[A]/GJCTGCCTGGCTGTTGGCTCTCGCCTTGCTGTTTTTGGTTCTT TCTCTTCTACTGGCTTTCTTTGCTTTGCTTGGCAGCCACCTATGCTGCTGT ACTTTCTTGAGCTGAGCAACCTCATCATCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG CATTGAGGATA[C]/TATGGAAGGCTCAGGAAGACTTCATTCTCAA AGGTGACTGGAAATCAGAGGCACAGACTGAGGAAGACAGTCATGGTCGAACA[A]/GJACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTCCATATAAA
WI-8837	63	A G	---	---	ATTTTATAGCCATGTTGGTAAAGTTCAITTTTCAGTACATGGGTAAACACCCAGGCCCTTTCCC[A]/GJT TATATCCAGGTATGCTACAAAGTTCTTTAACTCTTATCAGAAGTTATTATTACTGTTTCCTTAGAGAG GCTACACAGGCTAAATTCACCTAGTTGGTTGTCTAATGTCTCATTATTTATCCTGAAGCTCGTG GAGGGACTTAACCTTTGGCCT[A]/GJCTGCCTGGCTGTTGGCTCTCGCCTTGCTGTTTTTGGTTCTT TCTCTTCTACTGGCTTTCTTTGCTTTGCTTGGCAGCCACCTATGCTGCTGT
WI-8850	21	A G	CTTTGGCCT	CAACAGCCA GGCAGG	ATTTTCTTGAGCTGAGCAACCTCATCATCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG CATTGAGGATA[C]/TATGGAAGGCTCAGGAAGACTTCATTCTCAA AGGTGACTGGAAATCAGAGGCACAGACTGAGGAAGACAGTCATGGTCGAACA[A]/GJACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTCCATATAAA
WI-8853	79	C T	AGGATA	AGTCTTCTGA GCCITCCAT	ACTTTCTTGAGCTGAGCAACCTCATCATCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG CATTGAGGATA[C]/TATGGAAGGCTCAGGAAGACTTCATTCTCAA AGGTGACTGGAAATCAGAGGCACAGACTGAGGAAGACAGTCATGGTCGAACA[A]/GJACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTCCATATAAA
WI-8865b	52	A G	---	---	ATTTTCTTGAGCTGAGCAACCTCATCATCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG CATTGAGGATA[C]/TATGGAAGGCTCAGGAAGACTTCATTCTCAA AGGTGACTGGAAATCAGAGGCACAGACTGAGGAAGACAGTCATGGTCGAACA[A]/GJACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTCCATATAAA
WI-8865a	42	T C	CA	GGTAAGTCCGA AGCATGTTG	AGGGTGACTGGAAATCAGAGGCACAGACTGAGGAAGACAGTCAT[C]/GGTCGAACAAACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTCCATATAAA GTGCCACAAACCTGGACACCAACCAACAGAAT[A]/CJCTCCCGTCTTTGAAATTTCCATTAAAGAGCA CAATGGGGTGAATTATACCAGGGATGCTCCAATCGCTCTTC
WI-8895	32	A C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTGTGAAATAATAAATAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA[G]/CJTATGTCAAGTTAATAAACAATTTCTAAGTGTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTACACGGCAGACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCGCTCGCTCAGTCAACCCAC
WI-8456	93	G C	---	---	TTTCATCATCAAAAGTTTTCTTTCCATAGAAGAAATGGTAATG[A]/JTGTATCAGTGCATATTTCTATGGAAA ATTATATCTCAAGTAAGTAGCCTAGAAATCAGAGACAGCAGCTATGTCAAGCTAGTATACAAGTCA AAGACACAATGCTGCCAATGCA[A]/GJTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGGAGTGCAC
WI-8496b	157	A G	---	---	TTTCATCATCAAAAGTTTTCTTTCCATAGAAGAAATGGTAATG[A]/JTGTATCAGTGCATATTTCTATGG AAAAATTCATATCTCAAGTAAGTAGCCTAGAAATCAGAGACAGCAGCTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTC TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41	G A	---	---	TTTCATCATCAAAAGTTTTCTTTCCATAGAAGAAATGGTAATG[A]/JTGTATCAGTGCATATTTCTATGG AAAAATTCATATCTCAAGTAAGTAGCCTAGAAATCAGAGACAGCAGCTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTC TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28	A G	GCCAGC	AACGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGG[A]/GJTCCCTCTCTGCCGTTGTCAACCCACATCCACAGAGCA GCCCTAGTGCAGGTGCAGCCACTGCCACCCACGGCACGGAACAGGACCCATGCTGCTG

WI-12108	40	C T A T A	TGAAAAGGG TTAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAAGGGTTAAACTCAAAATATC/TJGAAATACITTTTCAATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTAA
WI-5989	29	G A C A C A G G C A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAACGTCCACAAAGGTCACAGGCA/GA/CJGTACATACGGTCTGTATACCCCATATATTAC CCCTTCATGTCCTAAAGAAGACATTTCTCTTAGAGATTTTCATTTAGTGTATCTTTAAAAAAAAT CTTGTTAACTTGCCTCATCTTTTCTGGGTGAGGACACC
WI-12201	61	C T C T G C A T G	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGCTTTTAGCCTTTTCTCGAGTGTATGTCCCAAGCCACTGATCACCTGCATG/CJTGCCA GGTATGGTGGGGTGTGATGGACGTGGGTTTGCAGCCCCCTCCACTGCTCGATAAAAGGC
WI-12018	31	A T T C T G A C T T	GGCAGCCAGC TCTGACTT	GGAGATGAC AGAAACAGAG AG	TTTTATCTGTCCAGGCCAGCTGTGACTT/JCTCTCTGTCTGTCTCTCCCCACATACCA ACTTCTCACCATGATGATTATACCAATAATACAGTTCTTATAGAGGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A G C C T C	TGGCTCGCTG CCTC	AGGGATCAA GAGAAAAGGC	TTTTGTGTTTGAATGATCCGAATGCTTGAGAAGAAACCCCTGGCTCGCTGCCTC/JGJGCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92	A G T T	CATGCCCTTA AGGATTAAGT	TCCTTTCTCTTT TGGTAGTGG	AGCATGTAAGGAGCAGTTTTTATTGATTGGTATATTACAGGTTTCTAACCCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAGTTTAA/GJCCACACTACCAAAGAGAAAAAGATTTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T C A A T T	GTTGAGTATTT GTTCTGCTCAT	GGGAAGGCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTATTCTGATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTCATTTAGTTGAGTATTGTCGCTCATAATTT/CJCCAATATGTACCAGACCTTCCC
WI-12326	25	G A C A	GACAGACTC AAAAGCAATT	AGGTTTGAAAA TATGTATTAAG TACTTTGT	CTGACAGACTTCAAAGCAATTCAC/GA/CJTTCCAGAATACAAGTACTTAATACATATTTTCAAAG CTGTTTGCAATTTCAAACAAGTTAGCGTTTTGTAAATCAAATTTGATAACCCGACTAAAAAT
WI-12361	63	C T	---	---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATATAGGAATTTTCAGCATATGTATTAT/CJ TGAACATAATTTACAAAAGTGGAAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87	C T A T C A C A C C A	CAGACACAGC ATCACACCA	GACCTCCCGT GGGC	ATACTGGTTTATCCATGTCAAATGTAGTTTACAAGGGAAAGGACAAGTACCTTTTGTATAGAATAT ACAGACACAGCATCACACCA/CJTAGGGCCCCACGGGAGGTGCGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67	A G T T T T	GGGAGGAAAA TCCAATAAAT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTCTGGTGAAATCTTTTAAAGCAGGAGGAAAAATCCAATAAATTTTTTAA A/GJAAAGGTTTAGCTATTCCCAATGCTATTTAATAACAATGAGGTAGGACGTTAAGTCTTATCAGA CTGTGTAAGTGGAGCCCCG
WI-11324	40	C G T G T G C C C A	GGATAAATCA TGTGCCCCA	ATCAAGCTTTG GGGCTCT	AGCATACTGCATCTCCTTATGGATAAATCATGTGCCCCA/CJGAGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTTATCTGTTCTGTCC

WI-11352a	69	T C G	AGCAGCAGC ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTCCAGAAGGAGAGAGATCATCTACATAAGCACAGCACATAGTGGAA AGTTC/GCTAAGTGTCTACGAGAGGTCAGATCATATCCATAGAAAAACAGCTCTCTTTTACTTGCACACTA
WI-11371	84	C T G	CAGCTTGGAG ATTCTGATTCA	GCCCGGCTGGA GCAC	TTAGCCCATGCTGTCAATTTGCAATCACCTGTGAACCTATGAAACTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTCAAGTTC/GTGTCTCAGCGGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTCGATCGGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCATTCT AGTCATGGTCA	CTTAAAGCATTATAGTTTGGCCTGATGGTGGACACAGAAAGACTTTCATATCTTGTGTTTTTAAAGTC TCTTCAGTTC/GAGGAAAAAGCTACAGATTTAAAAAATATGACCATGACTAGATAAGATCAGC
WI-11388	88	C A A G T T C	TGTTTGAAT ACACGTAAC	TGCCCTGTATC CAAGTTAAAT	TCATGTGCCAGTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAGAATGAATGTTTG AAATTACACGTAACTAAGTTC/CATATAATTTAACTGGATACAAAGGCAATGTTATGCTAAT
WI-11392	55	T G A T A A A T A C	GGTATGTGT CTTGAACCTTA	GTACATTCAAG TGTTTTGTAAA	TTCTATCATTCCTTAAAAATGGCAGGTTATGTGTTCTTGAACCTTAAATAACATG/GCTTTTTTACA AAACACGTGAATGACTTCTTGTGCAAGAGGGGAACACTGAGTCTCCGCTAGATCCATTAACTGT CATACTCTTCCCCAGA
WI-11396	52	A T T	TTTTTTTTG AAATGGTGT	AGCTTATTTTC ATATTCACCCA	AAAGAATAAGATGGCATTTGTTTCAGTTAATTTGTTTTGAAATGGTGTGTTTATGATGGGTGAATA TGAATAAAGCTTACCTCATCCCACTCTAAAAGGTAGTTGGTGAATTTTGAACCGTTGTCAAT
WI-11441	100	C A C A G C	TCCCCACCAAC TGAGAAGCCA	TGCCAGGGCCT TATTTG	CTGTGAGTCTTCCCAACTAAACCGTGAGTCCAGTATGTCTGGCAGCACGCTGTCTTGTCTTGGTG TATTCCTTACTGAAATCCCAACCAACAGC/C/ACAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAATGAAT
WI-11466	26	C T T T A T T T T G C A	TGAGAAGCCA	GTTTATTGTTA TAAAAATGAC	ACTTTGAGAAGCCATTTATTTTGCAG/C/CTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACTTCTATTATCTATTATCTCTCAGATACATTT CATGTATCTCTG
WI-13364	35	A G	---	---	TTTTCTTTTGTGCTCTTTTTTTAGTAGAAGC/G/GGAACAGTTGTCAATACTACCTTCTGTGTGG TCCCCTGTTAGACAACATACCTTTCTTTGAAATGTAAAAATGTCA
WI-11276	41	A G A G C A G A C	GGCAGCCAGG AGCAGAC	TGTAATGAGGA GGCGGTG	AGGCAACACTGCTTTATTAGCGCGGAGCCAGGAGGAGCAGAC/G/CACCCGGCTCCTCAGTACACATT CCCCACCCCTGCCCTGGTGTCTCCCACTCAGGGCTGGGCGGAGGCGGTAGGCTCTGGAA
WI-12210	76	A G A	ACTGGGAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC	ATTGGAAACAACCTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATACTGGGAAAAACAA CTATTGCAT/G/GGAAACATATGCAAACTAGCATCATTTGTCTCTAGA
WI-14186b	88	A G	---	---	AATGGTCTGGTTTTTATGAGAAGCTGTGGTCAATTTGATGGAAAGACACATACGGTACAAAATTACA GGTGGTTTATGTTTCAATACATG/G/ATACAAATCATTAGAGTCTTTACAAAGTCATTAGAGTCTTTGGAT TTT

WI-14186a	52	C T A	GGTCATTGGAT GGAAAGACAC	AACFAAACCA CCTGTAATTTT GTAAC	AATGGTCTGGTTTATTGAGAAAGCTGTTGGTCATTGATGGAAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTGA	ATTTTTTTGGCTATAGGTCAGTGGTTCTAAACTTGAGCTTGCAAGAGAACACTTGTGGGGCTT[A/ G]TTCAACATGGACTGATAGGTCCACCCAGATTCTAACTGGTAGGTCTGGGGTG
WI-12345	37	C A	GTGGCAGGAA AAAGAGGAA	TTGACAGGGG TTCAGG	GGACAGACCTGATCCACGTGGCAGGAAAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCTGACCAGCTGGGCTTGGCACTTTGTGAGATTGCAAAA
WI-13416	71	C A	AAATTTTGG AAGTTTTTCAG	AGTGTATTAG TTCAATGAATA ATTCAA	GAAAGGCTGTAATTTTATTTCAAATTTTGGAGTTTTCAGAAAAAATAAAATGACAAGAACA CATA[C/A]AAATATTGAAATTTATTCATTGAACATAAACACTTAGCAGAGGAAGGACTTTTGAT
WI-12310	46	G A	TTATTTCCAAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTTGGTCT AAA	TTTGAAAGATGCTGAATTTTATCCCAAGTATAATTTTAAAAAGCT[G/A]TTAGGACCCAAACATA TTTAAACATCTCTTACACATACAGAAATTCAGTTTACAAATATCCAGAAGGCATTTTCTTAAAGCAG T
WI-12086	72	C T	CCGGGAAAC TTGGATT	GGAGTCTCGG GTCTGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAACAAAAACGTTTCCGGGAAAACTTG GATT[C/T]CCAAAGACCCGAAGACTCCTCCAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGCAGA ACAGGAACATGCCCTTAGCT
WI-11549	102	T G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGTCTCACAGGTGTAATTTGTTAAGAGTTTGTCTATCTAAATTTTCATATTTATTGGCATAAAGT TCATAATATCTTTTATGATCTTTTAAATATCTG[T/G]GGGGATTGTACAGACTTTCCCTC
WI-11585	79	T C	TGGGTTTGCAA AAACAAAA	CCATGCTTCAG TGATACCTCC	TTAGAAGGAAAGAAATAAAACACGGTAATGGGAAAAATCAGTTAGAGGTAGGAAGGAGCTGGGTT TGCAAAAAACAAA[T/C]GGAAGTATCAGTGAAGCATGGCCTAGAAAGTCCAAAGCAGGAGGTAGAGT TT
WI-11604	68	G C	---	---	TTAGTTGGTTTCCCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT G/C]AGAAGTGGGACTTTCCATGAAAAATAATTAAGAGCTAAGGAATTTCTGACGCTCACCAATTTTTC TTTGTACTCTGCAGTT
WI-11614c	108	C A	---	---	CAAAATCAAAAAATTGAGGAGGCAAAAGACAGAAAGTAAAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60	A G	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAAC ATGCC	CAAAATCAAAAAATTGAGGAGGCAAAAGACAGAAAGTAAAAATCCAGAAAGACTCAGCTGCTTG[A/G]GG CATGTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83	T C	---	---	TTGATTTTACTAAGGTCTTCCACTGGAAACATGAAGGTAGGGATAAGGTACAGGATAATATACTCAG ATAATTTTAAAAATAAA[T/C]TACTTAATAATAAGAAATTAGCCATACCACATTTGTTCCATTTTGCTAC AAGAACAATTTGGCAATGA



WI-11626a	39 G A G	T C C A C T G G A A C A T G A A G G T A	G T G G T A T G G C T A A T T T C T T A T T A T T A A G T	T T G A T T T T A C T A A G G T C T C C A C T G G A C A C A T G A A G T A G [G/A] G A T A A G T G T A C A G G A T A A T A C T C A G A T A T T T T A A A A T A A A T T A C T T A A T A A T A A G A A A T T A G C C A T A C C A C A T T G T T C C A T T T G C T A C A A G A C A A A T T G G C A A T G A
WI-11627	23 T C A T T G C C T C	C C T T C C T T C C C A T T G C A A G G T A	C A T T T G C A A C C C A T C T C A A G	A C C C C T T T C C T T C C A T T G T C C T C T [C/G] C T T G A G A T G G G T T G C A A A T G G G A A G T A A A A G C A A A A A G G G A G A T G A G A A A T A C T G A T G C C T T T T T G T C T G G C T T A C T T C C A T T C G C A T G C A A G T C C A T C C A T G
WI-11636	61 A G T C C T	G G A C T T A A A A A G A T C T G C T T A	A G A A A C T T G C T A A A T A T T T T A T	T C A G A A A T G T T G C A A G C A A A T A C T A T T T G T A A G G T G G A C T T A A A A G A T C T G C T T A C C T [A/G] T A T A T C C A C A T A C T C T A G T G T T A C A T A A A A T A T T A G C A A G T T T C T G T G A C A G G T G C T C A G T A A A C A C T T T G A C T C C T T T T T G G T A
WI-11537	119 C G T	A T T G C T C A T C T T A C T C T G A C C A	G A C C C A G C A A A A A G A A T G A T T	G T A C C A T T T C T A T G T G G C A A A T A A G C A A A C T G T G A G T A A A C G A G G C A G C T G A A T A A A T T T A C A G T A T A C A A T A T T A G A G A A T A T T A T G T T G C A A T T G C T C A T C T A C T C A G A G T T C A C A C T C A T A T T T C A T A T T T T T T T G C T G G G T C C A G G A C C
WI-11654	37 G C T G	G C C A A A A G A C T A T T C A G C A A	G G C T C C C C A G G A C A G T T T	A G T A G A A C A T C A G T G C C A A A A G A C T A T T C A G C A A C T G [G/C] A A A C T G T C C T G G G A G A G C C A C T C C A G A G C T A T T T C T A A G A C T T T C T G T G G T T T C A T A C T A C T A C T C A G A G T T C A C A C T C A T A T T T C A T A T T T T A T T T T G G G T T G G G T
WI-11656	28 G A A A	A T T G A T T T A G A A G G A A C T G C	C A A G G C T T T G T C C T C A A G T A A A	A C C T G A T T G A T T T T A G A A G G A A C T G C A A [G/A] C T T A C T T A G G A G A C A A A G C C T T G C C T G C A G T T G T T T A A A T G T C C T G A A C A A T C A G A T T C C A G C C T G G A T
WI-11680	55 T C ---	---	---	A C A G A T A C T T T T C A C G C A A C A T T T C T G A A A T G A A A G C T T T G A T T C T C C C C T T T T [C/T] T G C A T A A A G G C T G G G A A G G T G G T T T G G C C A G A C C G T A C A T C T T T T
WI-11696	47 T C A G G G A C A G	T T A T C A C A G C A G G G G A C A G	G G C A T T A G A G A A G C C A A C C T T	G T C C A A G A C A A A A G A T A C T T T G A C A T C T T T A T C A C A G C A G G G G A C A G [T/C] A A G G T T G G C T T C T C T A A T G C C C A C C A C T C T T G T G T T T C A G A A T C T T T C C A C T T C G C C
WI-11702	69 C T C A G C A G	G A A T A A T A C T G A A A T A A C C A	A G A A C A A C T T A A G C A A A T T A T A C T G A A A	T T A C A T G T G T C A A T G G T G A C A T A C T T T C A A T A A T T A A A A A T C G A A T A A T A C T G A A A T A A C C A C A G C A G [C/T] T T T C A G T A A A T T G C T T A A G T T G T T C T A G A A A A C A C T G C T A A T T T T G T T T C T G C A G A
WI-11706	60 C T T C T C T T C T	T G G C T G G A A T T T T C T C T T C T	A T C A C C A A A G A A C A A A T T C C A	T G C T G A T T C A T C G C T T C T A C C A C T G G C T G G A A T T T T C T C T T C T T G T A C A A T T A T T T G C [C/T] G G C T G G A A T T T G T C T T T G G T G A T T T G T C C C C T T G C T G C T
WI-11709	105 T A T T C A G T T T G C	A A A G C T T G C A T T C A G T T T G C	T C A T T T C T T C T A A T T T A C G G G A	A A T A T C A C T C A T A T C A G G C A T G T T T A T A A A A T G A G A G A T T A T G T C C T T T T T G G C A T A C T T C A T C T T C T T C A G G A C A C A G A G A A G C T T G C T T C A G T T T G C [T/A] G T C C C G T A A A A T T A G A A G A A A T G A A T G G C C A G A T G G A T G G A A A A
WI-11710	103 C A C A G T C T T C A	G C A C C T A G C C T G A G G A G	G T G T G G A G G A G G G A G G A G	T T A T T A C C A T C A A C C T G T C C C C A G C T T T C A G C A C A C A G C C C A C A C T C T A G A C A G C C T T C A C T C C A G T C C A T T C T G G C A C C T A G C C T C A G T C T T C A C [C/A] C T C C T C C C T C C T C C A C A C A C T C C T T C

WI-11715b	123 C T	AGCTGGCTGC AGCTT	TCCCATCTCG TGGCT	AGAATGGAGCTGTGGGAGGACATGCACACAATGTAAACAGACAAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGCTGGCTGCAGCTTC/TAAGCCAC AGGATGGGACTGGGAAGA
WI-11715a	49 A C AAA	GCACACAATG TAAACAGAC	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAA/AC/TTGCATTACAACCTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGCTGGCTGCAGCTTCAGCCAC AGGATGGGACTGGGAAGA
WI-11727	43 G C TCAACA	AACAATCCTT AAACAACATA	CCTGTGGTTTG TGTTGCAG	CTGGATTTCCTATACCTAACATCCTTAAACAACTATCAACA/G/C/CTGCAACACAAACCACAGGC AAAATGAAAAACAGATGCCCCAGACAGACACCCACCACACATGGCACACAC
WI-11728	16 C G ---	ATCTGTGGTTT TCGCCG	---	TTTTATTATCAAACTC/G/CAATTCCTATTCACAAATGTAGTTATCATCAGCTCCCATCCACTTT CTCCCATCTCTTATCTCTTTCCACCCCTACACTTCTCTCCCTACAACCCGGTTCCAAA
WI-11758	61 A G TCGCCTG	GCCTCACAAA GTATTTCTAA	TGATTGGCCCT GTGGTCTA	TTTTCTCTTTTATTAAGTCGGCTATACTAACTAGAAAGGAGATCTGTGGTTTCGGCTG/AG/CTAG ACCACAGGGCCAAATCACCACAGCTTCTGTAGAGAACATGGAGATGCCAAGATCACCATCA
WI-11295	37 A G AATATAA	GGCTCACAAA GTATTTCTAA	AAAAGTGCTCA TCTGTGAATC T	CCGGCCCTCACAAAAGTATTTCTAAATATAATTTGCT/AG/CTAGAGTTACAGATGAGCACTTTTCA CATTAGGTGATATGCAAAACAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93 T C ---	GCCTCACAAA GTATTTCTAA	---	AGCATGATATTCGCTGGAGTTTCTGTGAGCTCAGCAACACAGAGTCAGAGATTAAGAATT ATTTATGCCCTCCTTTTCTCCCTTC/CTGTGATTGTTAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42 C G GCAAGGGAA	GGCTCAGAGA GCAAGGGAA	AAAACTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTTTATTAATGGGCTCAGAGAGCAAGGAA/C/G/CACACAAAATTTACAGTCTGA GTTTGGGGGAGAGACCCCTCTCCACCTTTTTCATGCCTGTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28 A G AAACCTCTG	CCCAACTTACC AAACCTCTG	CGGTAGGCGAG GCTAAGC	TAATTCACCAACTTACCAACCTCTGT/AG/CTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAAATGGCAAAATCATCTAACACAAAAGC
WI-11879	61 C A AGTATACA	TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACITT ATAAAA	TTTTAATTCCTAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG/C/AGT GATTTCTCTCTTCTCTTTTATATAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91 C T AAGTTTAAA	GTTTTAAATGT GGTATTAGAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTACTAATTTCCATTCCTCCCTTTTATAGTTTTTAAATGGTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATCTATTTCTA/C/TTTGACAGCACAGTTCTTCAAAAGTTTGCATAGACAATCTGA AAATGGGTTCTGAAC
WI-11906	52 A GATCTGAA	TGTTATAACAT CAAGAAAGA	TTAATTTCTGC AGTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAGAAAGAAATCTGAAT/AG/TTGAGGGAACTG CAGAAATTAACCTTCAGTCTAATCTCAGATGCCAGAGTAAGATGAACCTTTTACAG

WI-11909	78	A G	TTTGTGGG TGGTCAAG	CTCTCTGAG ATTTCTGAAT AG	GCAGTTCTCTGAAAGACAAATGGATTGTGGAGCATACTGAAGACTATTCCTAATGGCTATTGTGTG GGTGGTCAAGTATGCTATTAGAAATCTCAGAGGAGGACAAATGATAGTGCAGCTGCAGCCAGCTCG GACTGGCTTGAAGATC
WI-11806	60	T G	CATGAAGAGT GGCAGTTCA	TCCTGTAAGC CAATTTTATAT ACTAATAA	AAAATACCAATTTAGCATCAATGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCAIT/GJGTT TTATTAGTATATAAATGGCTTTACAGGAAGCATTATGG
WI-11946	31	C A	---	---	CCCTAGTGAATACAACTTTGTCTGGAGACIC/AJCCAGCTAGTCTAAGAAAACCTCCTAGGCTGAG CTCTCTGGGAATCTAAGATAAAGAACTGAGATCCTCTGGGAAGGGAA
WI-11965	65	T G	TGAAGATCAG ATCTCTGGTT ATTT	CAGCTGTGGT AATGTTGAT	ACAAAATTCACAAGTACAACACTGCTTATTTCTGCTTGAAGATCAGATCTCTGGTTTATTTAAIT/ GIATCAACATTCACCACAGCTGAAGGAATTAACCTGAACCT
WI-11027	90	T A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTTATT	ACCTATTTGAACTGCAGAAAGGCGAGGACAAACAAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAT/AJATAAAAACTGTAAACACATTTCCCTCATTTCTTACGA ATACITTTCTTTTGATATTGCAATTTCTATGGCATACACAGAGGCACTCCTCAATGCCCTG
WI-11049	95	C T	---	---	TTCTGCTGAAGATCACAAAACAAATTTCAACCTCTGTGGTTCAAAATAATTTAAGGATCTGTACCTTT GTGTTATTTCTGTTTCAACTAAGGA/C/JAGACTTCAAGAGGATAGCTCCCTTGTAACGTTTTT AAACATCTTTTCAITTTGAGGAAGGAACATTTCAAAAGCCCA
WI-15488	69	C T	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGGAAAAAGTTCTCACTCTGCACATATAAAAAGGACAGCCAGATATCA ACIT/GITACAGAAATGAATAAGATGGAAAAATTTTAAACAAATTG
WI-13654	49	A G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGT/AJGJGATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAAGGTAACTTTTCCCATTTTACAGACAAAACCCAGT
WI-11070b	135	C T	---	---	ATGAGACCTGCTTTGAACGTTAAACGTTTGGATAATGGAAGAGGAGCTAGGACAAATCTTGCTT TCAAGTAAAAATGTGACTGAGCAGAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAAAGTA CIT/GTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-11070a	110	G T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCTGCTTTGAACGTTAAACGTTTGGATAATGGAAGAGGAGCTAGGACAAATCTTGCTT TCAAGTAAAAATGTGACTGAGCAGAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-12020	121	T C	---	---	AATCTTTATATTTCCAGCTGTGAGACAGTATTTTGGGGCTGATGTTACCTCTAGCGGCGAAACC AGAGCCAGCTATTAAGCAGCCAGAAAGCTACAGTAATGAATACATGACCATTTT/CJCTCTTTTAGC ACGTTCTTGTCTCCTC

WI-11076b	142 G A ---				CATGGTTCTGCCAGCTTACAGGAAGCATGGTGTGGCATCGGCTTATCTTCTGGAGGCCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGAGCAGGAGAGAG AAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCTCAT G
WI-11076a	106 T C AGGCA	AAGGGGAGC	TCCTGCTCTGG GTATGTGAC	GGTTATTCAAA AATTAGTATGG GACA	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGTGGCATCGGCTTATCTTCTGGAGGCCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGAGCAGGAGAGA GAGAAAGAGAGGAAGTCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCTCAT G
WI-14263	49 T C GGCATATTCA	CGCAGAAAAA			ACCTTTAAAGTTTCTCCCCACCTACTCCCGCAGAAAAAGGCATATTCAA[T/C]GTGCCATACTAAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA AATTATTGCTGAAATTAGGAAGGAGCAT[T/C]GAAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAAGCAAGTACCATTTTCCAAAGTATAAACTCGTA
WI-14267	28 T C ---	CTTTTCATTTT TGCTTTTAAA			GATTTGTTTTATTTCATCTCGCTTTTCAATTTTGTCTTTTAAATAGAAC[G/A]CTTTGATTTTGTAGTA TATGACATCATCATCATGAATTTTCTCTTACTTTGTATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-13892	50 G A TAGAAC				ACCTCTTTCTGATGACACTTGACTGTAAAGGGTCTAGAGAGAAAGAGTAGTACTCCTACTTTGCT TACAATTCAGGATGCAGGGCATGAGAGGATTCCTCTCTC[G/T]CCAAAGGGAAGAAAGCTTTTGGC AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAACAGACAGCCCCAGATCAGAGGAAAGAGATG GCTTTCTTGTTAAATTCTGGAGCA[G/C]ATTCAAGCAGCAATATTTACTGAACACTTGCTATGTGCTG G
WI-13951b	88 G C ---	GGAGTGAACA AAGTAATGAA			AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCAGATCAGAGGAAGAG ATGGCTTCTTGTTAAATTCTGGAGCAGATTCAAGCAGCAAAATATTTACTGAACACTTGCTATGTGCTG G
WI-13951a	39 C T CAAAA	AAAAAGGCTC TTGCCCAT	TTCTCTGATC TGGGGTCT		GAGACAAAAAAGGCTCTTGCCCAT[G/A]TATCCCGTCTCTCCCTCCTGACTGACCCCAAGTGTCTT ACAATGAACATCCCTCAGCCCCATGGCATGGTGCATCCCTTCTCTTGGGATCTGTGAATATAACCA ACTGTCTTGTCATGGC
WI-13264	25 G A TTGCCAT	AGCAAAAGGA AGTTAAATAC			TTATTTGTCTATTAGCAAAAGGAAGTTAAATACTGATAGA[A/C]GATGCAAAATTTGTCTTTTCATGCA TTTGTGGAGCAAGTACTAACTTGTTCACGTGTCATTTCCCTCACAAGGAGTTGAGCCCCCTAGATGAC
WI-13960	39 A C TGATAGA	ATCTTATAAC AAGAAGCCTT			AACTCTTTATTGTTTAGCTAGCCCCAGTACTTTATGCTATCTTATAACCAAGAAAGCCTTCAAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATCACACTTTGTCTCAGGGTCCACCAGGAACCCAGGCTTGGCT
WI-15843	62 C T CAG				

WI-13983	52	G A	TCTCTCCACT CCTTAAACCT	CAATACCTCTCT TAGCCCACTGG	TTGTGTATCTGATTTCCGAAACATAGAAATCTCTCTCCACTCTCTAAACCTTG/AJCCACTGGGCTAA GAGAGTATTGTACAGAAATATGCACACTACTGACTTAACAGAAATAGAACATCCAGGCACTCACTGAGA
WI-13850	51	A G T T	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTTTAACACAGCCATTA/GJTTACAAACATTGT CAGGGAACATTTACAAGAAATAAATAGATGGAATGCAGGTGTAAAGATTACACTTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCCCTG	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCCTGATG/CJTTTCCCTTTGCCAACTATTCATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAGGCCCGAAATATGAGTGAGACTCA
WI-14284	55	C T ---	---	---	ATTTCAAAACAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA/CJTTTATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85	G C C C C A G A T	CCGCTGCTATT CCAGAT	GGTCTCTTCC ACCAAATCTT	ATGACCAGACCAAGCCCTGTCTATATGAAGACAACAGGTGGCCATACCTTGGGTGGAGGGATA CCGCTGCTATTCCAGATG/CJAGATTGGTGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33	C T A C A A C	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTTGATGTAGTTACCCCACTAATAACAAC/CJTGAGAACCACTGACTTCAAATATTATGAGAG AAATTTACTCCAGGGAATTTTGCAGAGAAGATAATA
WI-13529	42	T C T T A C C A	CACAAACATT TATTGAACAG	TCTATACATT CTCACTCTCTT	AAATATGATTCCATCCACAACATTTATTGAACAGTTACCA/CJAGCAAGAGAGTGAGAAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGTCTCGAGGGGTTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84	G A ---	---	---	TTATTTGTCAGAAATTTCCAGAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAAGGAAACTATG/AJACAAACAAGTATATATTCAGGAAAGGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T C ---	---	---	TGAAAGGATACAGAAAAAATCAGCGAAGT/CJGAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAAGCTTCCAGTTGTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52	G A ---	---	---	TTTTATTGTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCACG/AJAACCTGTCGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTTGACGCCGGCCCTTGAATCTGACATTTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13477b	61	A G ---	---	---	TTGGTTTTTAATACCTCTGTGGATAAAAGGAG/CJCATTTGTTTTTCATTAGCTTGCTTCAAAAGAC AGAGAAATAAGATAAAATTACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A G A A G G	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTGTGGATAAAAGGAG/CJCATTTGTTTTTCATTAGCTTGCTTCAAAAGAC AGAGAAATAAGATAAAATTACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTG AGAAACATTTT	CTGACTTTATTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATATATGTCAGTTATAAAAAAT GTTGGGTACTTTTCCAAG[A/T]AAATGTTTCTGAATGTGCACACTAGAATATATGCAGAATCCTTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTTACCATTAAAGAAATCAACA TGTGCACAAAAAGAGTAAAAAT[T/G]ACCAAAAAATTAAGATTTTGGGACAAATTCACATGTTT AAAAAT
WI-13582	43 C A AGACTGGGA	TGCAATCTAG	TCTGGCAGTT AGATTCCA	AAGGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[C/A]TGGAAATCTAACTGGCGAGAG AAATCAAGACCGATGGTGAATCTGGGCAGCTTCAAAATTTCTGCCTCCTAAAAACATTTTCAC CCAAATTTTCATTATGGC
WI-13857	28 A G ---		---	TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTTAGGTATCTGGCACAAATTAACCAATGT CTGCCCATTTTGTGTAGCTTTCATACAGTACAGATTTCATTGATGCTGCCACATCTG
WI-15809	77 T G TGTAATGCC	TGTTTTCTGT TGTAATGCC	TAAGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCC[T/G]TTTACAAACATTGAATTAGTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T ---		---	TTAATCAGTCTGTGCAAGAAGAAACAGGACTTGATCAAGCTTCCAGCCCTCACCAGCTCTATCAGCA TAGCAATTTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAAGGA[A/T]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCCTTTATTCCAAGAAATGGGAAGC[G/A]CATTTTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACT CTAGCTGCAGTAATACTGCATCCCATCCACTCTCTCTCTTTTGTACTGAAACTCTTCAAAAGAACT GCTGAATGTCCTCTCTC
WI-15801a	24 G A AATGGGAAGC	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	GCTGTAATGAGACAGAACCGCTACAATCTGTTCAACACTGGCTGGACACTGCAGTGAT[T/C]AGGG GCAGGTGTGGGCAGGGTGGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13763	59 T C GCAGTGAT	GGCTGGACACT GCAGTGAT	CCACACCTGC OCT	TTTTTTTTGTTGAGTGTGTTGTTCTCAATAAGAGCAGAGAAACCTT/AJAGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATTGATATTTTGGCTTTTCCCGAGGGGCAAAAAAGA GAGCTCTCCAGAAACCTC
WI-13578	48 T A AACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGTAAG AACATCTTTT GTC	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAAATGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCTCCTACTCTTT GAGGTCCCT
WI-13789	62 G A AGGGAG	TGGATGGCTG	CAGTGGCTTC CTCTGTTT	
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCTTTGGOCA GTACTTTT	AATAACAAGTTTAAGTTTCAGCTGCAATGTTGGCAATGCAGGTTTTTAACACAGATCACAAAAAGC[ G/A]TGACAAAAAAGTACTGGCGCAAGGACAAAAATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40 C T ---			GTCTCCCACTACTCCGCGCAGAAAAAGGCATATTCAA[C/T]GTGCCATACTAATTTTGAATAA CCTAACTCTCCCTTGTCTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACACTGAA GACTCACCAG	TCCCACCCCA CCCT	GTCTCACTTCTTGTCTAGGCTGTAAATTTTCAGTTTAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCAGAA[C/G]AGGGTGGGGTGGGAATACTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCCT
WI-13600	26 G T	TTAATGAGCC AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACITTTAATGAGCCAAGCATCCAT[G/T]CCATCATCTAGTAACAAATTTTCAATATGCACATTATAT TATACTGGAACAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCAACCATCAGCAACCCTCT TGATTCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAATATTTA ATATTAAT	GATAGGAAAAAGAAATGAAGTCAATAGTCTTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCC CTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAAATATTGTCATGAGGTATGCACCT GCCC
WI-13650	76 A T	AAAGATTCAC AATATTTCACT TTTAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAGATTCACAATATTTTCAC TTTTAAAC[A/T]TAAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAAAGTTACCGG
WI-14319	83 C T A	CAATCAAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTGGGGTGGGACAGTACAGAATT
WI-13528	80 A G AAAA	CAATACATTT GCATTTTCCTA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAACTGTAACTAATCAATACATTTTGCATTTTCTTAAAA AAAGAAGACATTT[A/G]TTCAGAGAAAACTGTGGTATCATGCAGGAAAAAGCAGAAAAAAT
WI-13909c	93 A T ---		---	ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT CTCTTCAAACTCGAATATCTTTTTC[A/T]GAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TTCTCACACT CTCTTCAAAC	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT CTCTTCAAACTG[A/A]AATATCTTTTCAGAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A ---		---	TTTTATTGAATCCAAATGTAGCAAAATCATTAAACAAATTTATAAAAGGGACAGAAAAATTAAG AATCAACATCATCTCTGGAC[C/A]ATGGGAACCTTGAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-14323a	78 T C ACATCA	ACAGAAAAAT TAAGAATCAA	GCCTTTTCAAG GTTCCCAT	TTTTATTGAATCCAAATGTAGCAAAATCATTAAACAAATTTATAAAAGGGACAGAAAAATTAAG AATCAACATCAT[C/T]CTGGACCATGGGAACCTTGAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-15389b	104 G A AAA	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCCACACTT	AAAATTGACAAATCAACTAGCTTGTCTTTTGTGTTTGGAGACTACCATTATTCAAATTTATATGT AATACACTCATCCAGATAATGAACATCTGCGAAAA[G/A]AGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33 G A TC	AATCAACTAG CTTGCTTTTGG TC	TTTGAATAATG GTAGTCTTCCA AA	AAAATTGACAAAATCAACTAGCTTGGCTTTTGTG[C/GA]TTTGGAAAGACTACCATTTTCAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAAGAGTGTGGAAATCACCTCATCTGTGCG TGTAATCTGCTTACAGTCCCTTTGCAAGACAGACATATGTTTTGCATAAAGATATAAATTTGCTTCAT TTTAAACTAAATTTAGTGTTT[C/J]TTTAAATTATATGAACITTTTGGTGAATTATGAACGTGTACCAAAC C
WI-15747	88 T C AGTGTTT		TAATTT	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCTCTCTGTTAAGTGTCTGGATATATCTTGGCTTGCACCGGACACCTTTTACG GAGGGATTCGGACAAC
WI-13752b	117 C T ---		---	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCTCTCTGTTAAGTGTCTGGATATATCTTGGCTTGCACCGGACACCTTTTACG GAGGGATTCGGACAAC
WI-13752a	106 T C AGTGCTGA	CCCTCTCGTTA AGTGCTGA	CCCTCGTAA AGTGCTC	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCTCTCTGTTAAGTGTCTGGATATATCTTGGCTTGCACCGGACACCTTTTACG GAGGGATTCGGACAAC
WI-14339	102 T G TTAC	CCCAATCAAA CAGTACATGA TTAC	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACAGTACATGATTACTT[G/CGGTTTCCAGAAATCTGGATAC TGGATGGATGGATGAGGCCACCTGTTTCAACAAAACACGTAAATGGAATTTCACTGCAGCTTTAGAT TTCTTTGCCACGCTAGGAGCTTGTGTATGTGCTGAACAAAACCTGA[C/T]GCTGTGCTTATCTTTTC CTGATTCT
WI-13744	115 C T AAAACTGAA	TGGTGCTGAAC TAAACTGAA	GC	CCTTTGACTATATTGTTTTTCCAAAAATAGGACTATGTGTAGAAGAGAGAGCCCCGTACATACCTTAT [C/T]AACCATTTCAICCCACCATTTGTAAAAATCTCATCTTCTGGGTCTGGATACCTCAAAAACAGAT
WI-14061	68 C T ---		---	TTACAGTTGGATTAACTACACACTGAATATATCTGAATTAACCTATTTCAACCTTTTCATCCATTGAG C[C/C]AATTTAAACTCTTGCCAAAGTATCATGAACCTTACGAAGAGGAGATAAGAGATCTGATC
WI-15719	69 A C CATTGAGC	ACCCTTTTCATC CATTGAGC	ATT	TAATCCATCAATCTAAAAATCACACATACTAGATCAACACAGAAGTACCACAGTATGCTTTATTTTGCA GGTATTAAATGGTTCTCTAAATCGATACATCCAAAACCTT[C/JAGTTAGCAGCAAGCATCAGTTCTTC
WI-13810	106 T C AACTT	CTCTAAATCG ATACATCCAA AACTT	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAAAATCACACATACTAGATCAACACAGAAGTACCACAGTATGCTTTATTTTGCA GGTATTAAATGGTTCTCTAAATCGATACATCCAAAACCTT[C/JAGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27 G T CACA	ATTTTATTACAC ATTAACATTG CACA	GTCTTTTGATA TGTTGGCTTAGT TTT	GGATTTTATTCACATTAACCTTGACACAGTGTAGCAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAGAACAATATACATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA TCAAAACTGCACACTATAAAAGTGTCTTTAAATGCAGCAGCAGGAGATGTGAAGACACAAAATGAAC AAGTGC[C/GA]TAGTGACACATAGCTGTCAACACACAGTG
WI-13785d	72 G A ---		---	TCAAAAGTGCACACTATAAAAGTGTCTTTAAATGCAGCAGCAGGAGATGTGAAGAC[C/C]AAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACACAGTG
WI-13785c	56 A C ---		---	



WI-13785b	40	C G ---	---	---	TCAAAGTGCACACTATAAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACACAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACAACACAGTG
WI-13785a	27	T C TGCTT	AAACTGCAC ACTATAAAAG	TGTTGTGACAG CTATGTGTGAC T	TCAAAGTGCACACTATAAAAGTGCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACACAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACAACACAGTG
WI-13793	88	C G ATAGG	GGATTTTACAT TCAGCCTAGAT	GGCAGGAGGA TTTGTACT	AGAAACCAAGTATATCATAGGCCAAATAAAAAATAGTTTTTACCCCATTTGATACAAACATAAGGGATTT TACATTGAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCATAAAATCTATGACTTG
WI-13794	52	A G TTTCTTTCTC	TTCCTCACCCCT	AGATGGGCTC TTAACCTTGTA	TAGTCTCCTACAAATCCTTCAATCCATTTCTCTCACCCCTTTCTTTCTC[C/J]TACAAGGTTAAGA GCCCATTTCTTCAACAACAAAAACAACATAGAGCAAT
WI-15729	35	A G GTGAGACTGC	CTTTGAACCAT GGTGAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[C/J]GGCCTTTAGAAAAGAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAAGGAAGGGTAAGTCCCTGTTTGCAGCCCCGGGCTGCTCATTTGTTA
WI-13424	66	G A C	TGAGGTTTTTC ACCCTATTCTT	TTTTCTCCCC AGGTCTA	GTCTTTGCACAAGTCTCCCAACTGGTTGGAGTTTCCCTTCTGAGGTTTTCACCCCTATTCTTC[C/J]A JTAGACCTGGGGAGAAAAACACATGTGTAAAGTGGCTCAGGACATGAGGCAGGCCGTTTCAACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29	T C AATT	TCTTATAAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGTGCAGAGGCAATTT[C/J]GAGATCCCAGATTCAGCTTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAAATTTCTGTCTGCTTTTAAICTTGAACATTTTGAAGCACGAA
WI-13446	22	G C TCACCTCAICA	GCCATGTTCTT	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTTCACTCATCA[C/J]CCTCTCTGATTTTGAATCCCTTTCTGCTCTGTAATTTTCTTCTC TTCCCTTTTTAGGGCCTAGTCTGTTTAGAAATCTGTTTGTAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCCTAAT
WI-13725	56	A C TGGGTGCC	TGAGCACATA	CCTGCTGTCTC GGC	TCACACAAAGGCATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGTGCC[C/J]GCCCGAG ACAGCAGGATAAGTTTCACAAAACCTTGACCAGGCAGGTTAGAAAGCAAGGCATGGTTCAAGATG
WI-15702d	107	T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAA[C/J]GGGTTCTTTGAACAATAAGTTT TGA
WI-15702c	101	T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAA[C/J]GGGTTCTTTGAACAATAAGTTT TGA
WI-15702b	90	C T ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAAATGGGTTCTTTGAACAATAAGTTT TGA

WI-15702a	48 G C A A G	A C A A A A T A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A T G T T T A T G A A G A G A C T C C G A A C A A A A T A A A G G C T T T C A A A A A G [G/C] G G G T A A A G G G T G A G G A A A G C A T G T G A G A A A C T G T A C C C T G T A A C A A T A C T A T G G G T C T T T G A A C A A A T A G T T T T G A
WI-13831b	113 T C ---		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A G G A G A T T C A C A T A C T T C C A C T G A T C C T C C G G T A A G T T T C C T T C T C T G T A G A T G T C C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	56 G C ---		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A [G/C] G A G A T T C A C A T A C T C C A C T G A T C C T C C G G T A A G T T T C C T C T C T G T A G A T G T C C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13806	62 G A ---		---	T G A T T G A G C T T A G A A G G A A G T C A T G T T G A A T C A G A G A G A G G C C A A A A C T A G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86 A G ---		---	C A C A T T T T C A G C A A A C A A A T C G A G T G C A A C A C A G G T T A T T T C A C A T T A A T A T A A C T G G A T T T T T T G C A A A T A A A T A G G G A [A/G] T T C T C T T A A A T A A C C A T C T C C T C A C T T C A T G G C C A G T
WI-14373	95 A G ---		---	A G G C T G T T T T G A G G C T G A G G A C C C C A C A C A T G A C A C G T A A G A C T G T A C C A T G G T C A T G T G A T T A T G A C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C A C C T C C A A C G C C T T T A C T T T C A C A G C C T C T G C A
WI-14078	61 C T G C A A G A	A A G A A G T A A A T T A G G A A G A	T G T G T G C A T G T C T C T T A C T G C	A G A A C C G A G A A C T C A A A G A A C C A C A C A T G G T G T A T C A A A G A A G T A A A T A G G A A G A C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A G A A G G A C T T T A G A T G G T C A C G
WI-14083	47 C T A C A C T	A G A C T T G A G A G C T T A A A A C A	G C C T A C T G G A C C T C T A A A C T A C T G A	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A C A C A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T T G C T T A A G G T C T T A C A A G G C C A A
WI-14085	31 A G A A A A A	C A T T T A T T T C A T G T G T A A G A	C A G T C A T G T T C A C G T G C T A G T T	T G C A T T T A T T T C A T G T G T A A G A A A A A C [A/G] T A A C T A G C A C G T G A A C A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A C A A A A T A G C A T G T T G A T T A A G T G A A A T A A C A G A A C A G G A G G C C T T T
WI-12169	121 G C T T G C T T	A A T A A A A C T T C C T A T T T T C T T	G G G T T C T G A G G T G A A A G A A A A A	G T C A A A G G T T G C C A A A T T T A T T T C C A C T T A T C A A G A C T T A C A A A A T A T T T T G T T C A T T T C T A A A T T T T C A C C T T T A T T G C T A A G T T A T A A A A T A A A A C T T C C T A T T T T C T T T T G C T T [G/C] T T T T T T C T T T C A C C T C A G A A C C C C C T T A
WI-15705	50 A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T C G T C A A A T A C T C T A G A A	T T G T T T T A T T T G G G G A G A A T G A A G G A G G A G G A G A T T T T A G A C T G A A T C [A/G] T T C T A G A G A T A T T T G A C G A C T A C A G C T C T C T T T G T A C T A C G G A G A C C C T G C T T A T A G C C C C A A C A G G A A A T C C T C A T C T G C G G T T G C A G A C A G

WI-14379	102 C T	TCTATTAACA GGGTTATGTCA CACC	ATCATCTGTT TGAGGTTGACA ---	TTTATGCTGTGTTGTTTCTACTGGTGGTCTGCTGCTCACTAATCAATCCTAGTATGATTTTCTTT TACTTGTGCTTATTACAGGGTTATGTACACC[C/T]GTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAA[C/A]CCACCATTAACAAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCGCGAGGCTGGCGAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22 C A	CGCAGAGCTG CTGTATTTAAA	GCAGAGATCCA GACGCTTGT	ACCGCAGAGCTGCTGTATTTAAA[A/G]ACAAGCGTCTGGATCTCTGAGGGGCTGGGACCAGCTGC AGTGGGGCTCGGCACTGCTCTGCTCTCCAGGACTCTTCCCACACCCC
WI-15937	24 A G A	AAACTGAAAG GTATTCCTCC	GGCCTTTAAGT TTCTACGGTG	TGAAACTGAAACGTATTTCTCTCCA[A/C]ACACCGTAGAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGGCGAAAAGGAAGTTTCAGGTGATACAAGATGTCCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24 A C A			ATGTTTATGATCAATCCAAACATACAGTACAGGGGAAGGTGAATAGTAAGAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A/G]TATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAGCTCAGTCACTAG
WI-14124	92 A G		---	GACAAAGAGGAGGAGTTTCTGTAGTTCCAGCAGGGCCAGAGCAGTTATCAGAACGGGTTGTTTGAACCT GCATAGATTTTGTGACGACTA[C/T]GTGGCCATGCCATTCCTGTAGTGAAATTAATGAACA
WI-14125	88 C T	GGTTGACCTG CATAGATTTT	GGAATGGCATG GOCAC	GTTTATTTCTCACAGTTCTGGAGGTTAGAAGTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTTCTCACCATGTCTTACAT[G/A]GCCCAAAGAGAC AGAACAAGCTCTCTGGT
WI-14136	120 G A	GCCTTCTCACC ATGCTCTCACA	CTTGTTCTGTC TCTTTGGGC	TTGTTGTTGGCACCAGAAAAGCT[C/T]ATGTTCTATGTTATGTCACTGTACATACTGTAAACAAGACT GCATTAAATTTGTTTCTTATGATTGTTTCAATG
WI-14138	23 C T	TGTTGGCACC GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	GGCAGGTTTATTCATAATTTCAAACTTGGAAAGCAACCAAGATGTCCTTCAGTAGTAGTATTCA GACAATC[G/A]AATATTACTTAGCACTAAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-13551	74 G A	GACAATC	TAATATT	TTTTTAAAGAGTGCTTTCACATCATTTATATTGTTATGGCACACAAAACCTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGAGATAGAAGCCCTTCTTCAGATCA CCTOOC
WI-15953b	59 C T	---	---	TTTTTAAAGAGTGCTTTCACATCAT[T/G]TATATTGATTGCACACAAAACCTTTTAACTCCGTCAC AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGAGATAGAAGCCCTTCTTCAGATCA CCTOOC
WI-15953a	26 T G A T	TTTAAAGAGTG TCCTTCACATC	TCATCTGTTCT TGTTGTTTTTG A	TTTTTAAAGAGTGCTTTCACATCAT[T/G]TATATTGATTGCACACAAAACCTTTTAACTCCGTCAC AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGAGATAGAAGCCCTTCTTCAGATCA CCTOOC

WI-14631	82 G A ---	---	TGAATTCATGGACAGTTTGGCTCTGTTTGTAGTAAACCCCTCACAAGCACTCTGCATAGTCGGCTTTCTGCTCTCTTTAAAC[G/A]TGCCTGGTTCCTCTGCCCCAACTTTTAGATTGGGCTCTCAGGGCCTTGTCCTGA
WI-6053	24 A G ---	---	ATCACACCGTGTCTAAGAACAA[G]TCTTCATGTCCAACTCATATCCCCGGGACTTTGTCAACTGCAGTACACTCTCGCATTAACCTGGCTTCTGGAGGGAAGCCTCTAGAGCCAGGTAAGGGGTGCAGCAGTGGGGTATATCTGGCTGGCCAGTTGGAAACCACGGAG
WI-15964	99 T A CTGGAGGTA	GACTTCTCCAC CCTCTTGC	CAGAACTCTTCTGTGTATTAAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGAGGCTGCCTTGGGAGGTAGTAAGCTCTCTGTCCCTGGAGTA[T/A]GCAAGAGGGTGGAGAGTCTTGGCAAG
WI-12075	103 G A GGCAC	CCCTTCTTTC TCTTCTTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAAGCCAGGCAATACCCCATCAGAGACAGTGACAAAGACAGCTGGGGGCACGGGGAGG[G/A]GAAGGAAGAGAAAGAGGGGAGGAGCCT
WI-12179	96 G A TGGAGGTCA	TCGAATGACCC TGTAGATGC	TAATTTAAACACAGCCCTTCCACATAGTGGGTGAGGCATCTGCACATTTTCTTAGAAGGACATGAATAGTGAITGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCATTCGAGGAGGAACAG
WI-14651	49 C G ATTGT	GGAGATATTGA TCTCATTTAAA CTTATT	CACAAATAGTGAATTTATCTGAGCAAGAATCATTTCTCATTTAAATTTG[C/G]AAATAAGTCAGAAAGATCAATATCTCCCTGCTTCAAAAATGACACTCCCAATTTTCACAGGTAAACCCTGTTA
WI-14666	105 T A ---	---	AATGGGACTTTCAACAAGGGTTTAAACTAACTCTAAACAACCTCTACAACACATTCACAGAGCATATAACAAGAATTATTTACAGGCAGCTAATGTATTTAA[T/A]AACCATGAAAAAGAAAAAATTG
WI-13473	31 C T ---	---	ATCTAGATGTCAGCAATGGGCTGAGACTG[C/T]TGCTGGTAGATGCAGTGTGTGTATGTTTCTAC TCTATTACAAAAATTAAACAGAAATATGGCTTCGCTTTGTGCAATGTTTATATCACAGTC
WI-13967	103 A C AAATAAAAA	TTGTGTTTCA TCTCCTAAAAG TG	AAATTAATAGCAGCTCTGTGTGTGATTTTAAAGAACAGATAAAATATGTCATTCAGCAGTCATTTAAAAATAAAAGACTACAGATACAAAGGAATAAAA[A/C]CACTTTGGAGATGAAAAACACAAA
WI-14408	60 T A G	TTAATTGTGTA AAACTCATTTG TTACTTT	TTAATATTTACAGCAAGTTATTGCAACAGGTTGAAAAATGCAGACACACTATTACAGGCTG[T/A]AAATAACAATGAGTTTACACAATTAAAAATATTAAACACATACTTATGGGATTTGTTGAATGA
WI-13683	47 C G ---	---	TTTTGTGTTAAGAACAGCATTTTGAATAAAACCTATCTGCCCATG[C/G]TTTACAGCCCTTTAAATTTGTAATTTATATAGTCGTTTATGGTACATATTGATTGC
WI-13910b	63 C T CGTCT	CATTGAGATAA AGCACACTTAT CAC	TTAGAAAACTGATAAAAGCAACACAACCTTTGGGAAAGCACCATGGCAGCTCTTTGTGCTA[C/T]GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22 G A ---	---	ACATGGCAGATACAGAGCTG[C/G]ATCTTGAAGACCACCACTGACCAGGAAATGCCACTTTTACAAATCATCCCCCTTTTCATGATTGGAACAGTTTCCCTGACCGTCTGGAGCGTTGAAGGGGTGACCAGCACATTTGCACATGCAAAA

WI-16002	59	T C	GATAACATAA AATGATCATG CAGAAATTC	GCCATCTCCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTCATTC/GTTA AAAGTCAAGAGGAGATGGCTAATGCATGCTGGCT
WI-15361b	101	A G A	CCCACTTGAAC TCAAGTCATC A	AAACTAAAC CTTTGTGCGTA AAA	GTGGAATTTTATTAGCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTGTGCTATCCCACTTGAACCTCAAGTCATCA/GTTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAACCA
WI-14759	73	T C	GCGTTGACTT GTGCGG	TCCACACTGC OCC	TGAGTTACAACAATGAGCAACAAGTTAGAAAAATGGTTTTATTCAAACTTCTAGCGTTTGACTT GTGCGGTC/GTACTCAATGGGGGCAGTGTGGACGGGGAGGATTGCAACAGAGTTTCATACTG CAA
WI-12535	50	A T T A T	CTAGGAGGGTT GAGGTGTAGA TAT	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTCAGGTGGTGACTAGGAGGGTTGAGGTGTAGATATATCTCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATGCGGTTCTGTGTTATCAGCTGAGAAAGGCAGTCTCGCCATC TTAAAGACCTGCGCTCC
WI-13805a	112	G A G G G A A	AAAGGCACAC GGGAA	CTCAGCCTGOC TTGACC	TTCCATTCAATTATGCTTGGCTTACCAATTTTTATAGCTATTGGGAGGCAGGAAAGGAAATTTTGGC CCCAGAAACCATGAGATTGGTTCAGAAAAAGGCACACGGGAA/G/AGGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCIC
WI-12340	18	T C ---		---	ACACAATATAATTCATTT/CJGAGTGATTAAACCTATTTGTTGTTTAGAACCAACAAAACTAC AAGAAACATTTTCAAAACCTTTTTTTCAGGCTGA
WI-14808	52	T A C T A C C C T G T	ACCACACACA CTACCCCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACTTTAAGCAAAACAGTTAAAAAGTACCCACACACTACCTGTTT/AJAAAACTTTAAC ATTGTGATGCCCTCTGCATCAATTTTAGAAAAACAAAGAAAAACAACTGAAGGCCCATGTA
WI-14816	29	A T ---		---	AGTTAAAAAAATCGAGTCAGCATTTATTTA/AAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCCGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTTC
WI-12542c	71	G T ---		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG/G/TTAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70	G T ---		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG/TTGTAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45	C T T T T A A A	GCTATTAGGC AAACTGAACA TTTTAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTC/TTATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57	C T C A A A A A	GGATACAGCA GTAAAGAATA CAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATTCTAGAAACTGGGGATACAGCAGTAAGAATAACAAAAATCCTGC/C/TTCTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28 T C ---		---	TC TTG GAG GGTATAGAGGACAGAGTGTTC/CJGTTGATTTTCGTTTCGTTTCAGTTTGGTTGTCATT GGTTTTCGTTTTCGTAATTTGGCCACCCATATAAAAGCAGTGCCACCCAGAGGCAG
WI-14856	60 A T A A	TGGTGACAG GAAAATAC TT	TTTGTTCCTA CTTTTACAAA CTTT	ACATTCCTTATGATAGCAACAACATAAATATGATGGATGGTGACACGGAAAACTCTTAAT/ATJAA AGTTGTAAAAGTAGCAACAATAATTTAGGTATATACTATAAGTGATAGAGGATGATATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14863	61 G A ---		---	ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAAGGGCAATATTTTGTGCTG/GA/JAG TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACATATTATTGATTGGCCACT ACCTGGC
WI-14867	46 T C A	GACATTCCAA GGCTCTCTAAC	TGGGCTGCAG ACACTC	TTTTAATTAACGTAAAAAGGCAGGACATTCCAAAGGCTCTCTAACA/T/CJGAGTGTCTGCAGCCCCA TTGGCTTGAGATGTGAATGTGTTAACCCAGGGTGA
WI-14733	98 G A A	CCAAATTGAC AGATATTTCTGC	GATGAGTGCAG GCCATTTATT	ACGGAGTCGTCTCTGATGATTTCTTTGTCAAAAAATGTTTGCCTGATTCTAATCATGAAAGAACAATT AGAAAAAATCCAAATTGACAGATATTTCTGCA/GA/JAATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
WI-14898b	79 A C ---		---	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATAAGGTGCCACTAAGGAAA ACTTTCTCCAT/CJAAAGCTGCCTGCTGTGCACGTTGCCTGGCTTTTGTCTAACCCCTGGTGTGCTGCATCT GCCGTGTTCTGCTT
WI-14898a	50 A C CA	CATGTACAG AAGAGTTGTCT	AAGTTTCCCT AGTGGCACT	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGCTCAT/CJAGGTGCCACTAAGG AAAATTTCTCATAAAGCTGCCTGCTGTGCACGTTGCCTGGCTTTGCTAACCCCTGGTGTGCTGCATC TGCCGTGTTCTGCTT
WI-14907	48 G A	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGTATTTATTTCCGACATTA CTGTAGAGGCACACATTTGGACTCTGAC/GA/JATTCCTCTGCAGCAG ACATTTGTGAAGCTGCTGGTGGCACACCCCATCAATCAGTACTCTCTGCACACTGCAGAGGGGCCACATG CACGATGCTCACGTGTG
WI-14911	52 G A C	CCAATACATT CAGTTCCTGGT	CAAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCAGTTCTCTGGTGC/GA/JAAGGTCTCTTTC CTGGTTGCAGACAGATACCTTCTGTATCCTCAGATGGCAGAGAAAGAGAGGAAATAATCT
WI-14913	88 C A ---		---	CTGATGCTTTGACATCTGGGGCATTTGCTGTCTCTAGAGAGACTACTTCTCTCTGGGACCAGCCAAATTC TAGTGATAGTAGAGGACTCA/CJ/CCTGCACGTGCACCTTTTCATATACAGATCAACCAATCCCAAAAC CTACACCTCCAAACCCT
WI-14914	66 G C A	CTGGACACAG TTTTCTCTAGC	CAAGCCCAGGA CAATAAATTC	ATTTCTTGATTGGCTGTGTAAGCCTGTGAAGTCACTGCACATCTGGACACAGTTTCTCTAGCA/G CJGAATTTATTGCTCTGGCTGTGATGGCTTTCACAGC
WI-14926	49 T C ---		---	GTTATTTTCAAAATGACACATCCAGATTGAAATGGGCACCTTAGCGAAT/CJACTTGTGGACCACA AGACTGTCTGAGAACATGTTCAAAGACAGTTTCAAATAAAAAATTTCCCTTAATCAGGTCCA

WI-16083	89 C T	ATGTTTAAACA CAACATATC	TGGAAGAAGATT CCAGCCC	GCATCTTTATTACCACAGAAACTCATTATGTGCTTAATCATTTGTTTAATATATAATATAAGCATGTT TAACACAAACATATCAAGGATC/TGGGCTGGAATCTTTTCCATTCTATAGAAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55 C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTCTGTGTTCTGGAACAGCTCTCTTTCCACAGGAGGAGTCCCTCATGGATC/TJGCGGTATTG GTTGGTTGTGGTATTGGGGAGCAAGGAGAGCAA
WI-14946	47 T C	---	---	TCAATCTGAAGGTGTCAAAGTGGTCTATTTGCCCCACAGACATAACA/T/CJCTCTAAATCATCTCTA GATCAGGGAGTCATAAGGACCATTAAAGGCTCATTACACACAGTACTTTATGAAAGGATT
WI-15987b	80 A G	---	---	ACATTAAACACAGCACAAITTAAGGGGTCCCAACGAGGTGGTAGTGCCTTCCACTATGTGAGGACAC TAAGAAGATGGTCA/GJCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32 C T	CACAAATTAAA GGGGTCCCAA	GGAAGGCACTA CCAACCTC	ACATTAAACACAGCACAAITTAAGGGGTCCCAACGAGGTGGTAGTGCCTTCCACTATGTGAGGA CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56 T C	AGGAAACTG CTAACTTGTC G	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTTCTTATTGCCGTTCTTACAGGGAACAGGGAAGTGTAACTTGTACAGT/CJTCCAACA ACTGATGAAGATCATCTTCTGACCATAGCGAACCTGTAGGCTTGCTGTTCCCTCCAGCTGA
WI-16100	52 A G	CAAAAAGCTA TTTTCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAGCTATTTCTACACTTGAC/A/GJGTAATACTAG TTTTCTGACATCTCTGTTATCAACTCTCTGAAAATC
WI-14958	83 A G	AATAATTTAT CTCTTCTTTT CAAGGG	AATGCATTCT TTGGGTTTT	GTGATTGATCTGTAATTATTGGGATTATTTATCAACTCTAAAATTCGAAGATGAAAATAATTTATCT CTTCTTTTCAAGGG/A/GJAAAAACCCAAATGAATGCAATTTTCAGTTTCTCCAGGCTTTGAACTGC AGCAGAAAATCAAGGA
WI-14976	35 C T	GTTGATTGCT TCGTTCAAAG	TCAAACATAAT CTTCCATTCTA AGC	TATTTTAAATGGTTGATTGCTCGTTCAAAG/C/TJGCTTAGAATGGAAGATTTAGTTTGAGGAG GGCAGGTTTGGGGTAGGCTAGCGGGCATAGTGGCCACAAGAGATGCCATCTCACACCTGGAG ACGTCCATGAGCACTCG
WI-14981	31 G T	TCAGTGGTGT TATTGGATTT T	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTTT/G/TJTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80 C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCTCT	TGATTACATTTTTTAAATCATGCCTACCAGCCCCATCTAAGCCAAAATTCAAACACCACCTCTGCATTA AATGAAGCTGCAG/C/TJAGGAAAGCTGAGCACATAGCACCCCACTGATCGGAAAGAAACGTA
WI-15002	72 T A	---	---	AAATCTCTCTTTACACACAGATGAACCTTTAATAAATTACAATGCACCTGAAAATGCCCTCTTGA TTTTCTT/AJTTCAAGTTTAGCCCTCAATGGGCTCTCTCAAGGCTGGACCTCAAGGCCAGTT
WI-15000	90 GA	GACAGAAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGCTAAGTA/GJTAGAAGTTTGTGCAGAACTAGAAAACAAAAATCCACCT

WI-12323	68 G A	CACAATACTT CATGTACCTAT	CACTGGACATA TTCCTACCTG	ATTTGTTGATGGTTAAATCTTATCTCTTTTATACACAATACTTTCATGTACCTATGAATAAA G/AJACAGTAGGGAATATGTCAGTGCAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91 A T	AAGGGACGAT TTAGTATCTAA	GGCATGCCCC GTGTTTT	CATAAGTTGCATTTATTCACGTCACGCCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAAAACA/AJCAAAAAAACACTGGGACATGCCCTGAAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100 C A T	CTGCGCTTTAT ATTGGAATTTT	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTAGCACCTGAAATTTAGGGAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCTTTATATTGGAATTTCTA/C/AJAGAGACCCCATGGTCTCCCCAAGTGAGGAAGCC AGGCACTCAGCCCTTC
WI-14712	38 T A C A	TGAATGCTTCC AAGTACAAAT	TGAAAGTATGT TGTATATGGTA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATCA/T/AJCTCACAATACCATATACAAACATACT TTCAATCACAACTCAAAATATAAAATAACCTACAAAATCACATTGC
WI-13712	40 A C T C T A T T G	TTTACTTTGTT GTCAATTTTAT	CCATAAGGTCT CACACTTTTCT	TGGGATACCCCTTTTACTTTGTTGTCATTTTATTCTATTG/AJATTATAAGAAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGCAATATGCAATATAATTTGTTGTTTAAATTTATGCAT
WI-16163	35 C T A	TCTGGTGATGC AATTGAAATA	GCTGCCAATTA CAATTAACCTTAC	TCTAAGATTTTACTCTGGTGATGCAATTTGAAATAA/CJATTGTAAGTTAATGTAATTTGGCAGCATT GCCAAAAGTTTAAGAGGACTATTTCTTTAAACAAGACAGTGTCTGACATTTATTTCAGGT
WI-13453	88 T A T C	AATGCACAAA ATCTTGCTCT	TCAGATTTTAA CATCTCTTCT	TTTTTTTATTGTCATTTGAGTGTCTTTATTATATTGGAAATTCAGTGATTAACATTTGTACAAAT GCACAAAATCTTGCTCTTCTT/AJTGCTAGAAAGAGATGTAAAATCTGACCTAGTTGAACAGTCTT AATGAACCTCATTGTCCAT
WI-16167	58 T C G A T T T T	CGCACTCTAA ATTAGAGATA	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTCTGATATACATTT/CJCATCTT ATTCACCACGAGCACACCACGACAGTAGAACAGITCCACACCTGATAAATTCACAAAGATG
WI-14482	17 G A ---		---	GCAGAACCAATTAATAA/G/AJATCTGCAAGTTTCCCCAAGAACTCTGGAAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGATAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81 T C ---		---	TGTAGTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATCTATGTGTATCCCAGTATCATGTAC GCACTAAAAAAAAT/CJGTGTGCTTGTGCTGTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97 A C	TGAAGATTAA CCCAGAGTCGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTGTGTATCCCAACAAGTATACAGAATACTCTATAAAACCAACCCCAACCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCGC/AJCTCTCTCAAAAATGCACAAATTAAGACG
WI-15012	59 G T A T G T	GCAGCAAGAT TACATCAGTA	CTOCAAATAGC CTAGAGTATAG	CATGGCAGCAAGATTACATCAGTAATGTAATAATAACAGCTTTTTCATTGAAGCTTTG/TJACCT TACTATCTCTAGGCTATTGGAGTGTCCCCAC



WI-15100	74 G A ---		---	GTCAACATGTT ATATTTCTTT TAAGAC	TCATTACAGCAAGAAATACCCAAATTATTTCCAAATAAAGCAAAATTTGAACAGACTGGA GTGAGAAC[G/A]GGTTCCACCACCAAGCCCCTCAAGACAAGATGGACACGGCAGCTGTTCTGGGGT GCATTTCTAGTGGACTTTAT
WI-14492	92 A T AATTACT				TGGTACAGAAATGTTTAATTACAGCAGGGCAGTGATTCAGTTAAATAAATAAACCCTTTATTTT CCCAATATAAAATTACTAAATTAA[A/T]GTCCTAAAGAAAAATAAACATGGTGACAGCTTT
WI-12002c	89 T C ---		---		TCCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACACCCCAAAACCACATGGAGACAGAAG ACGAGACACAACCTCTCCCCAC[T/C]GCCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-12002b	68 G A ---		---		TCCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACACCCCAAAACCACATGGAGACAGAAG AC[G/A]GAGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-12002a	30 C G GGACACAA	TCGGAATCCA		TGGTTTTTGGG TGTTTTCTT	TCCTTAATTTTATCGGAATCCAGGACACAACACCCCAAAACCACATGGAGACAG AAGACGAGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-15116	96 C T GTTCAGTAA	GGGAGCCCTA		CCTGAATATGC AATTATTTATT ATGACA	TTTTCATTTATTTCCAGAAAAAGAAATCACATTTTCAGTAACAACCTTACATATAGAAATTAACATTTG TTCTGGAATGGAGCCCTAGTTGCAGTAA[C/T]GTGTCATAATAAATAATTGCATATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-12578	37 C T AATGGGA	GGCCTAAAGG		TCAAGCGACCA CCAACAC	GCAAAAGCAAAAGCTATGGAGGCCCTAAAGGAATGGGA[C/T]GTGTTGGTGGCTTGATACTTGGT GCTTGTGTGCATGGAGCAGAAAGTCTCCTGTGTCATGCAGGGGGTCACATATTTAACTGCACATAAT TTGGGCAAACTGTCATTG
WI-15153	40 A G GCATTGCA	CCCTTATGTTG		AACCTCAGATA AGTGCAGTGC T	ATTTACGTTGGCCCAAGATCTCCCTTATGTTGGCATTGCA[G/A]GAGACACTGCACCTTATCTGAGGTTA GAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTACCATTTCCTAA
WI-15215	84 G C TCAAAATGGG	TGGCTTTAGAA		CCAACAGGGGA AAAAGTCA	CCTTTGTCTCTGAACTGGGACCAGGATGTGAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTGAATCAAAATGGG[G/C]TGACTTTTCCCCTGTTGGTGGAAAACTCTGTGAGGGTTTGGCA
WI-15225	80 C T C	CTTGAGGACCT AGAAAGCAAA		TTTGATTGGCA TAATCACTCC	AGGAAAGAGTGGTAAAGCAAGGGCGATCATTGGATGAATGATTATGTGTACGAGCACTTGAGGAC CTAGAAAGCAAAAC[C/T]GGAGTGATTATGCCAATCAAAATTGCAAGGTTGGAGATATGCTAAAA
WI-15152	51 G A ---		---		AATTTGCTAGTGCAATGGACCCAGAAATTTGGAAGGGCTATGTAACACACA[G/A]TATGCACACCAC AGCCATGTCAGTGTACAGATCCCTCTGTGCATTGCTTTCCTTAAAAACACATCAAAAGGCTGCA
WI-15123	55 C T TAGGATG	TGTTAGTGACA GACAGATAAA		TTGCTTAAGGG CAACACAGAC	TGACTGTATACCAAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACCTCACTGGGGAAGAAACAGACATGCAACACGAGATAAAACACAAT

WI-15182	49	C A	GCACAAACCAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACTAGCTAGCTGCACAAACCAGGGCAAAATAC/AITGCTGGATTAACCC ATGCTAATGGGTTACCTTTATTAGTAATCATGGTCCCTCATAGCATGGTCCAGATCCG
WI-15198	38	T C	GGGCCCTTGGC ACTATG	ACTTATCCGTC AGCAGAGTAG	GTGGAOCTCTACAAGTACCATGGCCCTTGGCACTATGTC/CCTACTCTGCTGACGGATAAGTTGGC ATATGGTTCAGATTGCTTGTCTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42	T C	CATTATTGAG TATTCTTGCTT	GTGTAGTCTT ACATGCTTACG	TCAAGTGGTAAATAGCCATTATTGAGTATCTTCTGCTTTGATTC/CCTACTAGCATGTAAGACT ACACATTACGACCCCATCTCTCAAGAGGAAGCTGGTATTATGGAAAAACAATTTGTCAATTCAGAT T
WI-14510	104	A T	TGGCAAAATA TGCATAACAA	TTGAAAATGGT TAAACTGGCA	ATGTTGAGAGTAATAATGCCCTACATATTAGTGTAAAGTACACCCAGATATTTTGGGGAGAAGAG TTGTTTGTCTTTTGTGGCAAAATATGCATAACAAAAATATTTGCCAGTTTAAACCATTTTCAAGAGT
WI-15239	57	T C	CATTGCAAT AAACACCATC	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCATTTGCAATAAACACCATCATTC/CCTGAG TCCACAGATAAGGTCCCGGAGAAAGGGCTTCCCTCTCTTCTCGCTGGTGGTTCAGCTTCCACGGAGT GAAGCCTTTTCTGGAATG
WI-12634	52	T C	GCATCATG AACTGTCTAGC	GGACAAATTGT AAACATAGCT	ATGAGTTATAAACTGGAGACAGCGCATATATGAACGTCTAGCAGTATTATTC/CCTACTTAGCTA TGTTTACAATTTGTCTGAAGGGTCTAGATGTGTACACCCAGAAAGTGGTGAATCTCTGA
WI-15249	34	T C	GGGCTTGACAC AAAGTTCTAA	GGAAAGCCAG AGATTTTAAAC	TTTGCTGAAGGGCTTGACACAAAGTTCTAATCTTACCTTTC/TGTTTAAATCTCTGGCTTTCCCTGGCTGG TGAGGAGCACAGGCTGGGCTTTCAGGTATCCAGTGGTGGCCCGCATCTGTTCCCTCCACTCCCTCCAG CCACATCTTGGCTCT
WI-12159	28	C T	AAGACACCGT GCAAATGC	CCCTCTCCTCA GTGCACITT	CTGTCCGGGGAAGACACCGTGCAAAATGC/C/TAAGTGCACCTGAGGAGAGGGGGTCTGTGACTC CCAAACCCTCGAATATTTATGAATCTAAGAGTCCAGACGCGAGTTCATCCACGGAGATCTGC
WI-12648	41	A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC	TCCCCAGATTGTATGGAAATGCCCTAGTGGCATTAAGGATGC/C/TAAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACACTACTCCATGTTAGGTGCTTTACTTGGATTATCTCACTTAAACCCACA
WI-12684	64	G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCACTAAACCATGCTGTAAACAGCTGTGC/G/ TCCATTAGGCTTTGTTGTTCCATTAGAGAGCACAGGAGGAAATTTAGCATAATCTT
WI-15260	75	G A	AAAGGATGAA GCTAATCATG	TCTCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGTCCACACAGCGGACACTGTCATAAGTGGAAACAAGGATGAAGCT AATCATGGA/GA/GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGAAATTA TCCCTG
WI-15325	39	T C	CATGTGGCTGG GAGGC	CCTTCCACCAT GATTGGA	AAGTTTAAATGGACTCACAGTTCCATGTGGCTGGGAGGCT/C/TCACAATCATGGTGGAAAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGAAATGAGAGC
WI-13936	123	C T	AGTTGGCATT AATAGCCTAT	TGAAACTCCCA CATGGATT	TATTTAGTATTTTCCATGGCGCTTCTCACTCCCTATACATCTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTTCAAGACCTATGACCTGTATCTTCAAGTTGGCATTCAATAGCCTATC/C/TAAGTCCCATGT GGGAGTTTCATAATAA

WI-14528	62 T	TTTTAACTTT TCTGGATGGTA T G TAAAT	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTATAATATATTTAACTTTTCTGGATGGTATAAAATTTGJTT GAATTATAAAATTTTAAATTTTATAATAAGTCTAATCGAGACATCACTGGGTATAATTGA
WI-15347	74 C	GACTCAAAG GAAAAGAACA T AATT	TCACCTCCCCA AGTCTTTG	TATTTCTTCGGTTCCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTTC/TAAGAGACTTGGGGAGTGAAGCGAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA CG
WI-14546	95 C	CCAATTTCTAG TGATAGTAGA A G GACTCA	AAGGTGCACGT GCAGG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTGATAGTAGAGGACTCA/C/CTCGCACGTGCACCTTTTATATACAGATCA
WI-15353	37 G	...	...	TTTATTGGCTGCTCTGTAATACAAATGTGGTGAACAC/G/ATCTTAATTCAGGACATCTTCCACCTTG TTTGGCTTCCAGTTGACTGCAAGACCAGTGTGAGGACATAGGCTGATTAATCAGTGG
WI-14580	100 G	CATTCCCATCT A GTCTTGCA	CCGACCAAGAT OCTOC	AGAAATTTTCTCTTTTAAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAATAC CTAGTTATTATACACATTCCTCTGTCTTGCA/G/AGGAGGGATCTTGGTCGGCTTAACA
WI-8540	73 T	GGCCTGCATTT C GGCTTA	GGCCTTCTTT TCAGGCAC	CCAGCTGGAGGTGGAATAAATCGGGCAACCACAGAAAAACACACAGCTACACAGGCGCTGCATT TGGCTTA/T/CJGTGCTGAAAAAGAGGGCCGACCTCTTGATAAAGAAATGTCT
WI-8039b	97 T	...	...	AAGTAGAACACAATAAGATGGCTCAAAAATATCAGAAATGCACACTACGCACATCACGAGTAAATACTG TTTGGTAAACTTGTTCAGTTT/CJAAATATGTATGTGTCGGTGCATGTCAATTAATATCCTTCT TACCACAGTCACCTAAAGAACCAAGCTTAGGACTAGGACACACACCACTGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTTAAATGCGCAGCCGACACCCACA
WI-8039a	87 T	...	...	AAGTAGAACACAATAAGATGGCTCAAAAATATCAGAAATGCACACTACGCACATCACGAGTAAATACTG TTTGGTAAACTTGTTCAGTTT/CJAAATATGTATGTGTCGGTGCATGTCAATTAATATCCTTCT TACCACAGTCACCTAAAGAACCAAGCTTAGGACTAGGACACACCACTGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTTAAATGCGCAGCCGACACCCACA
WI-8044	107 C	...	...	CACAACATTCAGAAATTTTCTGCAATTTGTGCTCTCTGATGTCTAAAAAGATTTGAGCTTTGACTAT ACGATTTCCACACTGAACGCAATTCATAAGGTTTCTCCC/C/AGATATGGATTCTCTGATGATTAATA AGCCCCGAATCTGGCTAAAGGCTTCCACATTCAGACATTTGTAAGGTTTTCTCCAGTGTGGAC TCTCTGGTGTGCACAGAATGGAATCTGGCTGAATGCTTTTCCACACT
WI-8550	32 G	GGGAACATCA A TGCAACAAG	TTTGTGGCTTG AGTTTACAAAT T	CTTACTACATGGGAACATCAATGCAACAAGTA/G/AAATTTGTAACTCAAGCCACAACCTTAGTTA ATAATCATGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCTCAGTGAA
WI-8057	87 T	...	...	TATTAGATAAAACCTTTGTCCCGATTCAAGATGTTTAAATTTGCTTCTTTAACTCTGTGACTTTT CCTGGTTCAAAGGACAGT/A/GATGGACAGCAGCAGGAGGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTGTGGCTCACAACCTGCCCTGTGAGAGGGATGCTGCCCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGGTGTGAAGCAGCCAGATGTTAAGG

WI-6192	91 A G	GACTGCTAAG GATTTAAATTG GAT	TGAAGTGTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAATTAGCTCAGTCCACATGATTGGCAGTTGGCATAATTCTAGTGAAGCAAGTGTCT GACTGCTAAGGATTAAATTTGGATJAG/ATTTTAACTTAGCCATCTAACACCTTCAAGCATAAC
WI-6194	105 T A	CACATGGCAA TGATAATAAA GAAA	TCATCCTCAG AGTGTAGTCTG CA	AAGTGATGTGCTCTCACAAATACATTTCTCAAACTCAAAACATCATGCTTGAATAATCACTGAACCTT GTCACCAAGAAGTCCACATGGCAATGATAATAAAGAAAT/ATATGCAGACTACACTCTGAGGATAG AGCTCTAAAGAGTAAAAACAATGGAATTTGGAAAAAATAGGAGTAA
WI-6213	164 C T	---	---	CATATGCTGCTTTATTTCTGTAAGGATACACTGAACGTTAGATGATAATAGCTAATGACAGAATGT AGAAATGAGGATCAGCTTCTTAACCACTCTCAAGAAATGTTAGTATGTTTGTTCATTACATGTTT ACTTTGATATTGCTCATTACTATGT/CTATATAATAATAGTAATACAGTAGAGGTGATCC TGCATTTCAGGTAAAGCGTAGGTGGAAATCCAGATTTCCCTTGAGGAAAA
WI-6217	131 C T	---	---	CGGGTTAAGAAATACCTTTAAATTTAGGTAATAAAGCTCAAGGAGTGGGGCTGTCATCTGTGGTG TCAGTCTTCTGGCCCCCTGGCTGTCAGTGTGCTCCAGGGCCTTGACAAGCAGCTCATTCAAG[C/T] GGCCACCATGGCCCTAGGGTGTCTCAAGTCCAGCAGCAATCATGGCTTCTCGTATATCTGATCC AC
WI-6238	175 G A	---	---	ATAGTCTTTATTTGTCAACGAAGGCTACACGGGATCACTTCTGGTTTGTGTTTTTATGCTTTTTTTTC TAGAAGGTATCTACATCTGCATTTATTTACAGCCTTGTGGTATTTACACAGTCAAGATACAGTGTTA GAAACACAAAGTGTGAGAAAAAACTTCTCAAAATJG/AJGTTCCAGACTTCAGGAAAAATGATT TCCACATGTTAAGGCCAGAGTCTCCAGTGTGGTGTATCCAGAAAGCAGCTTG
WI-6272	86 C T	GCATTTATTCA GGGAAAACCT TAA	CTGTTTTTGA GAAAGACAAAG AA	CTTGATTTAATCAGGGCTTTGGGGTCATAGGGGATTAGTCACTGTACAGTCATAATAATGCATTTA TTCAGGGAAAACTTTAAJTC/TTTCTTTGTCTTCTCCAAAAACAGCTGTGGAACACCTCAAAATTA GGGATGTTTCATCTAAACACCTTTTACTGAACTTGATTCCTTGGGCCAGAGGAGGCTTTTACTGTAG CAGAGGACTTAATGCAATGCCCTATTCCGGGCAATAAATGAATACTTGATGCATTCACAGGCAAGAA TCCCAGCATCCAGAGAAAGCTGTGTG[C/GA]CTGCAAGGCATGGCTGCAGACATCAGGGAAGCT GGTGCAGTTCTAGTCTCGCCTCCTCGATTCCCTGOCAGCAGTCTCTCTCTCTCTCTCTCTCTGCCCC TCTG
WI-6303	96 G A	CCAGAGAAG CTCTGTCTGC	CAGCCATGGCT TTGCAG	ATGCTTTTGCATGATTCTAATTATGCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCCTTTTCAAGCCCAGCGTGTGCATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTGTCTCCATGAAAACTGGATAAAGAGTTGCTGATAGTGT[C/T]CTGGTT CTTCCCCTTACATCTTTTGGGGA
WI-6315b	193 C T	---	---	ATGCTTTTGCATGATTCTAATTATGCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCCTTTTCAAGCCCAGCGTGTGCATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTGTCTCCATGAAAACTGGATAAAGAGTTGCTGATAGT[C/T]AGTGTCTCTGGTT CTTCCCCTTACATCTTTTGGGGA
WI-6315	187 T C	---	---	CTTCCCCTTACATCTTTTGGGGA

WI-6375	28 A G A A	GGTTATTGCA TATGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTATTGCATATGGAAATCAATAGAGTATCTTTTACAAAAAAGGTTAGATAAAGATCTC ACATTTGTAAAGGCACATATGAACATTTTATAGCAAGCACAAGGCGAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTTTTCTGATAAGACAAATTCAAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA[T/A]GCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ---		---	TTGTGCTCAACAGATGAAATTCATAACCTTGTTTTCTGATAAGACAAATTCAAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	CTAATATAATCCTGGGCACATGGATTCCAAGAGAGATTTTGCAGCAGATTTCAATTATAGTTACTTAA CAGCTAAATAATAAGGGTGATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]ATCAACCTTCCCTAAGCATCTGCTGTCG
WI-6523	165 G T GCTG	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	CAGC TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGAAACAGGAAGATGGGC TCTGGAGTCCAAACAGGATGTGGAGTCCCTGGTAGTCTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAAGTGAGCTTCAACAACACGAGCTAAACTCTGAGAGAAAAAC[C/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G ---		---	ATTGTAATTAAAAATTACATGGGCCTATTATTAAAGGACATTGTGTAATGTTTCCACTTTGTTTTAAA [C/T]AATTACAAACATGTGGCTTAAAAATAATGTACAGATCAATGTAAACAGTTTGAAAAATGGGCG
WI-6558b	68 C T ---		---	ATTGTAATTAAAAATTACATGGGCCTATTATTAAAGGACATT[G/C]GTGTAATGTTTCCACTTTGTTTT AAACAATTACAAACATGTGGCTTAAAAATAATGTACAGATCAATGTAAACAGTTTGAAAAATGGGCG
WI-6558a	42 G C ---		---	AACCAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTTCAGAGAAATAAA AGTTGTCATA[T/C]AGCAATGGATGCTGTGTCAGAACATACTGCCAATAAACTTTAAGAAAAAAGGA ACTCAATGAAGTTACTGTATATAAAACAGGAGCTCACAGCAGGATGTAAAGATTAAATGGAAGAT ATCGTGAGCCAAAAC
WI-6629	75 T C GTCATA	TCITTTTCAGAG AATAAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAAAATCAATCAAACTCCAGCTGTTTCTCTTGCTTT TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCAATTTCTCAAGCACA T/CJACCCAACTTGAAGGTGATTGAACCCAAAATAATGGTGGGAAACACCAAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGGCCAAAGCTATCTGTTATATTTGATGTTGCCAAT
WI-6644	134 T C ---		---	TGCTAAACACCACCATTTATTAAAGGAGAGTACTAGGAAAAACTCAACACAGCATGTGAAACAGT TGGGCACGGTGGTAAAGGACAGACTCTGGAGCCACAG[C/T]GGCTAATACACTGCAATATTTTA TGTTTAGCAAAATTATAGCTGGTCTGTGTATATAACCAAGAGCGGTATCTGG
WI-6690b	106 C T AGCCACAGC	CAGACTCTGG	TAGCC	

WI-6690a	28 T C A G A G	AAACACCACG ATTATTAAGG	GCTGTGTTGG TAGTTTTCT	TGCTAAACACCACCATTAATAAGGAGAGTCJACTAGGAAAAAATACCAACACACAGCATGTGAAAC AGTTGGCAGCGGTGAAGGGACAGACTCGGAGCCACAGCCGGCTAATACACTGCAATATTTTA TGTTAGCAAATTAAGCTGGTCTGTGTATACCAAGAGCGGTATCTGG
WI-6770	53 A G A A C A T C A C A	CAAAACCCAA AACATCACA	GCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAATGACACAGATCTTCCCAAAGTAATCCAAACCCCAAAACATCACAAGJAAATTAATTCAT ACTATTATACACTCCAAAGCAAAATACCTCAACTGCAATCC
WI-6886	151 A G A	GCATTCTTCCA AAAACAAAAGA	CCITGTAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTCAGCAATCAGTACACTAATCTTGACCAAAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTAAATTTAGATGAAATTCACATTTAAACATGTTAACTCAAGCATTC TCCAAAACAAAAGAAJGJAAACATTGGAATAGTCACTTACAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGAATG	AAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAAATGGJAJCTTCTTCTCTCCAGCTTTTGTGAACAAAAC AATCTCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTGTTTTCAGGTACAAGGTCTC
WI-6844	225 T C		---	TAAATACTGCCAACTAGCATTACGTCCTCTTGTCATCATTAAAAACAAAGGATTTTCTCCTTG GTATTTTCAAATGATGCATTATACAATAACGAAGTTAGAATTTAAATGCACCTGATTAATATG TAACTGGTAATTTGTTTAAAGCATATAATTTGGTCTCTTCTCATAAAATGGAATTTTAA TATTTCTCTGATAGCTTGAGGTTCJATCATTATGAGTAGTGCAAAAGTGTG
WI-6824	112 A G		---	CGGTTTGTCTACACTTAATGGGTTTTTTTAAAGGATTTTTTTCAGGCTTGTGACCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGTACAGAGTGTGCCAAJGJACCTTAGAAAAATTACAT GACACGGAGAAATGCGCTCTTGTCTCTGAAAGCTACAGTCTAGGGATTTGACAACTCACAGT CTTAGGAACTGGGCAAGTAAGGCAAAATCTTCATCCCTAGAGCTATTGTG
WI-6889	139 T C A A T T C	GAAAAATGAG ATGCAGTTAA	TCACTTTGTGG CTTTAATTAT TCT	GTACAAAAAAGCTGAGAAGAGCCAAACATGGAAGTGTCAAGAAACATTTCTGATAGGTACGGACAA AAGAGCTCCTCAATCAAAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTCJGJAGAAATAATTAAAGCCACAAAGTGAAACTGTTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C		---	TCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACCTCAATATCTGATGAACCTGATGAACGTGAA AAGAGGTCTCCTTAAACAAGATATCATCTCCGAGAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAACTTTGCCCTTCCCAAGGAATGTGTTCTAATTTGGTTTCAAAGCACACTGGTTCC CACTTTTACCACCTTTCJCATGACATTGGACAATAGTACTACTCTTTCTAC
WI-9413	112 G C		---	GCCAGTCTAGTAAGTCTTAGGGACATGACCAGACCAGAGCCCTGTCTATATGAAGACAAAC AGGTGCCATACTGGGTGGAGGATACCGCTGCTATCCCAGATGJGJAGATTGTTGGTGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAAACAGAGGTATGA
WI-9557	74 C T		---	AAAAGCTTTAAAAAAGGTGGTGTATCTTTAGAAACACTTTCAGCAAGATCAAGTAGCCCAAGCT ACAGCCCTCTJGGTGCATCTTAACCCCTCTCTCTTT

WI-9617	37	G T ---				TGCTCTTTTATTTCACGTTTCACAACACACGCCGTG/GTTGGACAGTCTACCAAAGTGCCCGCAG CGCCACGCTTGGCCGGAAGGTCTATTCTGTCTCTATGGACTGATTGAATTTGGGATGGCCAG CTCCAGAATGTTCCACGTGGGGCACCTCTGTGGGCAGAGAGGCTAGCCCTGCCACACTGGCAACCA AAGAGGTTCACGATGACGCTTGACGTGGTCCAAAGCCGGTGTGCTGTG
WI-9657	121	T G ---				AATGCTGGAGAAAACATCAACATTGAGTTGACATTTGTTTGTGAAGTATAGCTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAAGT/GJATAATTCTT TGTAATTAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAATTAAATGCTTTTGATATAGATTGAGG
WI-13119b	114	G C GCTGGGA			AAAAATTAAAC CAGGTGTGGTG T	CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT(G/C)ACACACACCTGGTTAA TTTTTTAAATTTTGTAAAGATAGGCTCAGCTATGTTGCCCGCTCAAAAAACAAACCAACTAAC CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT(G/C)ACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACACACCTGGTTA ATTTTTTAAATTTTGTAAAGATAGGCTCAGCTATGTTGCCCGCTCAAAAAACAAACCAACTAA C
WI-13119a	51	C G ---				ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT(C/T)CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAGAAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACACTATGGCAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-13112	71	C T AGCTTTT			TTAGAAAATTTT GTGTATTATAT GGAAAAAG	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA(C/A)AAACAGCATCAGTAGTGTACACTTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAAAGAAAGCCCAAGGTCAGAAGTATAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCATCTTTATCTCCCTGTGGATGAGATGTATGCACACACAAGT AAA
WI-12988	36	C A CTCAGTACAA			CAAAGTGTACA CTACTGATGCT GTTT	TGCTATTTCATGACAGACACGTCGAGACAAATATTTCTATTTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCCACTAATAGTGGAAACCCCTGAGACTTTA(G/A)ATCTGCAAGGGGTTTAAAT GCAAAATACACATATATTTCCATTTTAAACACCATAATTTAAGTTTCCATTTTCTAATAGAAAAATGA TAAAAAATGTTTCCCAATAT
WI-13020a	108	G A CTTT			CATAATAGTGG AACCCTGAGA CTTT	TGTATAAAAAATCCAACTGTTCCACAAAGTACATATGTCCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAGTCCA(A/G)TACAAAAAACACAGCATTTCCCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAGCA AGTTGTGTCCA
WI-12837	87	A G AAAGTCCA			GCCATAGGAA ATGCTGTTTTT	

L42611b	50 G C ---			---	GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCCTGTCGTCGCTCTCCTGGCCTCTAG TCITCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTAGTGCCCTCACTTCTCTCTGTCTATAOCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTTGATTTTACATCATATGATTTCAACCA CTGGAGCTTCACCTTGTITAC
L42611	34 T C ---			---	GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTTCCTCAGGTTGCCTGCTCTCCTGGCCTCTAG TCITCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTAGTGCCCTCACTTCTCTCTGTCTATAOCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTTGATTTTACATCATATGATTTCAACCA CTGGAGCTTCACCTTGTITAC
WI-1172b	179 C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG		TGAACGTGTGGTTAAACTAGGCAATTGGTTAAATAATCAATTTAAAAACAGGCCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTTCTGCTTTC AAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAG[C/T]GTGCAGTGAAATAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17 C A ---			---	TGAACGTGTGGTTAAAC[C/A]TAGGCAATTGGTTAAATAATCAATTTAAAAACAGGCCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCCTGCAGTGAAATAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35 G C A	GCAGATTGGA AGTGTGAAAA	CACCTACATTT CTGAATATTTA GACTCTTT		AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTCTAG AAATGTAAGTGTGCTGCCCTCAACTGTTCTTTACCCACTTAATTTCTGCAATTTTGAAACTAGATTGAAT TCCTTTGCAAAACCCCTTGCAATCATGGATACCCGAGTTAAACCGTTAATTTAAAGACATTTAAACATGG CCTGGTG
WI-1231b	141 G A ---			---	TCCATGGTTTGGTTGCTACTGACTTGTAGCCTTACTGCCCACTATGCATTGGAACATTCCTCATATTTC CAACTAAGCAGGAGTGTTCACAATAAACACATAGGCTCTTTATCTCCTTCTTTCATTAATTTCTT TCAC[G/A]TTATTCCTCACCCTGAACGCCCTTCTTCTCTGTAGTACATTTTAAATCCACTTTAC ACATTCGGACC
WI-1231a	126 T C A	GGCTCTTTATT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA		TCCATGGTTTGGTTGCTACTGACTTGTAGCCTTACTGCCCACTATGCATTGGAACATTCCTCATATTTC CAACTAAGCAGGAGTGTTCACAATAAACACATAGGCTCTTTATCTCCTTCTTTCATTCATTCATTTT CTTTCACGTTATTCCTCACCCTGAACGCCCTTCTTCTCTGTAGTACATTTTAAATCCACTTTTACA CATTCGGACC
WI-472	114 G C ACAGAAAAG	ACATACATAT CCATTATACA	GACCTTCTTT TCCAGGCC		GAAGCAGGACTGTGTTTGGAGGACAAAAGTAAATCTTTTATCTTTATTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACACAGAAAAG[G/C]GGGCTGGAAAAAGAAAG GTCAAGTGAGATTTCAGATATCTTAAATGCAAGGCTGACAAAATTTGGGCTTGATT



WI-478	46	C T	GCATGCTGTG T TACTCTATTT TGTTCT	AAATGCCACAG GTGGCT	AAACCACCTGCAACCTTCAAGCATGTCTGTGTACTCTATTTTGTTC/TAAGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATCTGCTTTAAACACAAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29	T C	ATCAGCAG AGTACCTTTCT AACT	CTTCCAAOCT CTACACAATCT T	AGCCATCAGCAGAGTACCTTTCTAACTT/CJATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGA CTGTCTGTGGTATAATGACCCTGTGTCCAGTTAATCCA
WI-601b	112	T A	---	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGCGAACAGAGAGGTTTCAATTGACTCCTAAACTGAGTACT/CJAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74	C T	---	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGC/CJGAACAGAGAGGTTTCAATTGACTCCTAAACTGAGTACTCAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107	A G	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAAACAGACACCCCTGGCTTCTCACCAGTCCACATGGTGCCAAACAATCCCACATTCTCT ACATCTCCCACTGGCTGCTCCTTCAACACCTCACCAC/CJACTTGGCTTACCGGGAAGCATAAA GCCAAAGCATTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36	G A C	ACTGCTTGCTT GTTGATTTAAT C	TTATCTAATC CCACATGACAG C	ACTCACTGCTGCTTGTGATTTAATCAACCTAGCCG/CJGCTGTCATGTGGGATTAGATAAAATA AACACAAAAATGAAAAACACACGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACGTTAAAGAT AATAACTTCAA
WI-991	37	A T	---	---	TGCATTCAATTAGCACCATAATAACTCTGTACAT/CJCATTTATTGATTTCATTATCACAAAAAT TATGAGTGAGGGATGATTGTTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCAAAGTCACAAAGTTAGTGACAGAGCCGGGATTGGAATCCATCAACTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACACACTGACTCCTTTTCTCCTTTGAAAAACAAGGC
WI-1011	70	G C CCA	CAGTATCTGA AGTTTTGTCT CCA	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTTGCAGTGGATGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTTGTCTCC A/GC/JAGAAGTCATTTTGTAGGTGTTCTGGCGTTTTTGTACGTTTCCATTTCTTAATACACTGC CGTCTTAAGGGAGGGCTTGCAGAGCATTTATCAGATGGCTGTTTGTCTGCTGCTGCACTGAAG
WI-5381	178	A T	---	---	TTATGCAGAAAGTCCATGAGTTTACAGAACTCAAGGAAGAAAGGCCCTAGAGATGACACCAGAA ATGAGAGTGGCTTGTCTCATGAAATTTGGACAGCATGTTCCAAAGCAGAGGGGAACAGCATGGAGAAGA AAATCATACTCTATCCACGTGCAGAAACTGGCAATTAGTTTTGT/CJTTTACTAAAACACAAATGT TTAACTTGGGGTCCACAACAAGGATATGTTGGCAATGGTATTCTGTGATG
WI-5791b	76	G A	---	---	CTATGATTCCATCTAGCAAAAGCAAGACTATTGGATAAGTTTCAAAAGATGAGAACAGGTCCTA GAACCTCAG/CJATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAGGTA AAAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTGCCCACCTGTTTGT TAGGAA

WI-5791a	44	C G ---				CTATGTATTCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTT[C/G]ACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCCAAAAGGTA AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTCTTATTGGCACCCCTGTTTGT TAGGAA
WI-5406c	120	C T ---				CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C/T]TATGAGCCAC ACTTCTCATTTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAAAGGAAAGAAAGAGAGGCAA GG
WI-5406b	118	C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAAGT GTGGGCTCAT		CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C/A]CCTATGAGCCAC ACTTCTCATTTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAAAGGAAAGAAAGAGAGGCAA GG
WI-5406a	42	A G ---				CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAG[C/G]GCCACTTCCACAGATGCAACAG GCCTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCTATGAGCCAC ACTTCTCATTTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAAAGGAAAGAAAGAGAGGCAA GG
WI-5798	48	G C TG	TTATTCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAAGTATTT TCAAT		CCATTCTCTCTCCCTCCCTCTTATCTCCCTGTTTTTGG[C/AT]TGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTAATACATGCATAGTTCTATATGGGTATCA
WI-5415	54	T A TTT	TCTTCATGAAT TCATCTTTCAG	GGACTAATTCA TGATCCGATCT		CCTGCTAATAATAATTAAGCAGGATTTGTCTTCATGAATTCATCTTTCAGTTT[A/T]AGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C T G	TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAAG		TGTTTTAACCCAGGACAGCCTCCAGAGAAAAATCCAAGAG[C/T]CTTAAACCATAATTTTGTTTA GAACTCCTGTGCCAACCACTCTTGATGTGAGTGAC
WI-5481b	131	A G CTGCAGTCG	TGTCATTTATG	TTACTTCCAGG CTCCAAGTATT		AAGCCAAATTCACATTAGTTGATGAATTTGAAATTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTCAAGAGGAGTAGTATATGCTGAAAAATCTATTTTGTCAATTTATGCTGCAGTCG[A/G]A ATACTGGAGCCTGGAAAGTAAAGACTTGGCTATTTTCCAAATTA
WI-5481a	29	G A AATT	CCAAATTCAC ATTAGTTGATG	CCCATGCATTA GATACTGTAAA ATT		AAGCCAAATTCACATTAGTTGATGAATTTGAAATTTACAGTATCTAATGCATGGGCATCTGTTTTC AACTCTGTTTTCAAGAGGAGTAGTATATGCTGAAAAATCTATTTTGTCAATTTATGCTGCAGTCGAA ATACTGGAGCCTGGAAAGTAAAGACTTGGCTATTTTCCAAATTA
WI-5492	38	T C ---				TCATGAGTCTTTCTTCAAAGATGCTTGTAAAGTCCCAAT[C/G]CAAGAAAGGATCCCATGCGCCTAAT GAAGATGTACCTCCACCTTAGGATAATTTTGCAGACCAA

WI-5826	134	T C ---			TAATTTTTTTTCTCAATCCTGGAGCACACCATGCTCTTTCTATTTTCATGCTTCACATTTATTTTTT TTTCACCTTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATCTTTAGTCG TTTCAAAATTAAATGCCACCATAGAAATAATTTCTAACCAACGAGCCAAACAGCCTCACTCTTCCTT CCTGGTGCAATTACTCTTTACAC
WI-5546	40	C T A	CCCAATACITTT TTCAGGTGAA	CCTGTATTTTA GCAACATGGG	CCTTATAACCCCAATACITTTTCAGGTGAAAAAGGGAAAA[CT]ACCCATGTTTCTGCTAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGGTAAATCTTGATGTGGGAAATAT TAGAAAAATTAAGCGAGAGAGGCA
WI-5552	97	C T	GGCACCAGCCT TTTTAGAGT	TGCACAAATG CCAGG	TGTTGTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTGTGAGCGGGTATGGGT GGGGCTATCGGCACCAAGCCTTTTAGAGTCTCTGGGCAATTTGTGCACCTAGTGTGAGA
WI-5836b	161	C T ---		---	TAAAGTTGATTTAAACACTCTGTGCCCTCAATTTTCTCACCTATAAAATAAAGATAAGTATCTAAAA AAAAAGAGAGAGAAATTAAGGTGGATAGACATGAATAACTCTGATGATCTGTTGATCCCTGAA TCCTGCAATATACACATGATTCGAATGATCTTCCATTTTGAAATTAAGCTTTTGAATTTGTTTCCCA ATG
WI-5573	58	C T	GTTCATAAGG AGGTGGGA	TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATGCGTTCAACCTCGATGATGATGGCGTTTCATAAGGAGGTGGGGA[CT]TGACAC ATTACTCTCCAACTGTTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G A ---		---	CAGACCTTGGAGCCTTTGCTGTTTGTCTTCCACCTCACTCTTCTGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCCCTCTATGCACTGCGTCTATCTCTATATGGGCAATATCCAATGTCCCATTCG/A TTTTGGCAATTTCTGTATATCAACAGAGAGAGGAGGTTGG
WI-5850a	92	C T ---		---	CAGGACCTTGGAGCCTTTGCTGTTTGTCTTCCACCTCACTCTTCTGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCCCTCTATGCACTGCGTCTATCTCTATATGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGGAGGTTGG
WI-5612b	125	A T TTC	CTATTAATGA GCATCGTGTCA	TTCTCTTGAGA AACCTAAAC ACTG	TGCCGTGATTGACACATAGTTATCTGACAGTAAATCATTTACATCACAATAATCTTATTTCTGCCCTG TCACACTAAATTGCAAGCAATTCATTTGATTGACTATTATGAGCATCGTGTCTATTC[AT]CAGTGTT TTAGGTTTCTCAAGAGAAATTATGCTGTCTTCTCTGTAACCTCAAGTA
WI-5612a	44	T A ---		---	TGCCGTGATTGACACATAGTTATCTGACAGTAAATCATTTACATTCACAATAATCTTATTTCTGCG CTGTACACTAAATTTGCAAGCAATTCATTTGATTGACTATTATGAGCATCGTGTCTATTCACAGTGTT TTAGGTTTCTCAAGAGAAATTATGCTGTCTTCTCTGTAACCTCAAGTA
WI-5636	26	A C	GCCAAATTTTAT CCGCAATAAA	CATCGAGGACT TTGGGAA	TGAGAGCCCAATTTTATCCGCAATAAA[CT]TCCCAAGTCTCGATGGAGGCAATTCAGAATCGGG GCAGGGGAGGCAGAGGTGAGACAGATGTGAAGAAC

WI-5865c	103 C G ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAACTCTTTTTCATTATGCATT ACTGACTCACTCACTGCTCTATCAAAAATTAA[C/G]AAATATTAATATTTTATTTACAGAGAA CTCAGAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA GAGAAGACAGACAACATAAATCCAGG
WI-5865b	99 T A ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAACTCTTTTTCATTATGCATT ACTGACTCACTCACTGCTCTATCAAAAATT[A/J]AAACAAATATTAATATTTTATTTACAGAGAA CTCAGAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA GAGAAGACAGACAACATAAATCCAGG
WI-5865	165 T A ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAACTCTTTTTCATTATGCATT ACTGACTCACTCACTGCTCTATCAAAAATTAAACAAATATTAATATTTTATTTACAGAGAACTC AGAGCCAGAAAAATGACCAAGACACAGT[A/J]CCAGTCTCCATCTTCAAAAGGTCACAGTCTTC AGAGAAGACAGACAACATAAATCCAGG
WI-5874	76 T G ACAGAAAA	CATAGCATGG ATAATATTAT	CCTAGTAAGTT TCAGTCAATTG ATATGT	CTCAGACATTCATTTCATTAGTTGTTAATTTTGTGTTTCATAGCATGGATAATATATACAGAA AAAAAATTT[G]TACATATCAAAATGACTGAAACCTACTAGGTAGCAATTTGTTTGTCAATTTGCT CATGGAGCCGACGTTGAGCTCTCAGTTTTTCCATC[A/T]TTTTTCATAATTTACTCTCTTTCTGTC ACAATGTTCTGCTCGTATTTCAACTCTCATTTGCTGATTGGATGTCATAAAAATATGGGTGATTCT AGAAAAAAGTAAATG
WI-5752	36 A T TTTTCCATC		ATGAAAAA	TTAGCAGAAACAACAACAAAAATGTCAACACTGCAGTAAAGAAAGTGTTCCTCCGATAAATA[C/G]C CATTAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAACGAAAGCCGAGTTTCGATTACACACA GTTGCTGTTTAAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAA CATTGTTGAAACGAAAGCCAGTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760b	61 C G ---	---	---	TTAGCAGAAACAACAACAAAAATGTCAACACTGCAGTAAAGAAAGTGTTCCTCCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAACGAAAGCCGAGTTTCGATTACACAGTT GTCTGTTTAAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAA ACATTGTTGAAACGAAAGCCAGTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760	187 G A ---	---	---	AAATATCTGGCCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTT[G/A]GTGCAAGTTAGAT CCACCCCTCACTATTGAGAAGCTAAAGTGAAGACTACTCATTTCTCAGTCTTCTGCTG
WI-5944	52 A G GGAATCTTG	TTCTCACCATG GGAATCTTG	GGGTGGGATCT AACTTGCA	GAGTTTAAATGAATCCTGTTCCCTCCTAAAACCTCCTGTTCCCCCAACTTCACATTTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGT[A/C]TTTGTCTGTGCGGTATCTGCTCCAATCACCCTTTCACCTTTATTTCTCTATTAT GCTGAATGAACGGTTATATTACAG
WI-5967b	148 C T ---	---	---	

WI-5967	165 C T ---			---	GAGTTTAAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCTCAACTTCACATTGACGAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGTCTGTGCGGTAT[C/T]TGCTCCAATCACCCATTCACATTATTTCCTATTAT GCTGAATGAACGGTTATATTACAG
WI-6093	53 G C ---			---	GGGTAAAGTCCAGAGCCACAGGTGAACTCGCCGGTATTGAAGTCTTTGGGCCA/G/CJGTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTCCAAGTGTGCACTGAGCCCATTTGAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTTCAGCAAAACCTTGATTGACGGTGAC ACACCATGCTTCGAGAGGAATGAGG
WI-6141	80 T C AGGTACTT	CTTCTTAATTA AGCATCTACA		TGAAAACCCCA GACAGTG	GACTCTGTCTCAAGAAAAAATAATTGAAAAATTGAATAATTATTAAGCACCTTCTTAATTAAAGCAT CTACAAGGTACTTAT[C/C]CACTGTTCTGGGGTTTCAATCCTCTTCACCTTTTAGACTTCAGGAAATT CAGAAAAATGCATGAAAAACAGGATTGTTACATGCAGAGAAATAGGGGAGATAAAAATTTGTCTTTT CTC
WI-6450	45 T G TGTCACA	CCAATGACTT ATTCTATATCT		TTGTTTGAAT GTGTGGTACTT CT	ATAGGACAGTTTTTCTTCCAAATGACTTATCTATATCTTGTCACAT/GJAGAAGTACCACACATTTCA AACAGAGCCAGGCTATGCCAGGGTGGGATTATTTTCACGGTCATGGTAATATGCATGTAAAGACTA TTTTACTGGCCTCTTTTATGCATAAACAAAGGATTGGTCTATTCACAAACATGTGTCAATACAG CAGTTGTCATGTCCTCTGGTACTAGAATATAGTCTTTATAGAATATGGTTTAGAATAAAGCCACA AATTATCTATAAACACAACA[C/T]AAGGAACGAGGCTCAAAAGTGGAACAAAAACGGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA
WI-7466c	141 G A TTGTCCTGG	TTTTCACAGTC		AGTCGCATGCC AATTATAATT	GAACTATCCTTTAGTGGTCCACATTTTCTATTTCTGATCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCTATTTCAGTGAAGTATCATATAAAGACATGCAAAACCTTTTCACAGTCTTTGT CCTGG[G/A]AATATCTCACAAAATTAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCCCTT
WI-7466b	80 T C GTC	GACTTTCTGGG CTATGAAATA		TGCTTTTATG ATAACTAGTTC ACTGAA	GAACTATCCTTTAGTGGTCCACATTTTCTATTTCTGATCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT[C/J]ATTTCAGTGAAGTATGTTATCATATAAAGACATGCAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTTCCCTT
WI-9814	104 C A ---			---	TGCTTTTAAAAATAACAATGACCACCCTGACACCATAGTGTGCTCCATTTGCCACGCTTCTCCTC AGTAGAATAAGACAGGACTTTGCTGGTGTATCT[C/A]TTCTCCTTCAGAAGAGCACTTTGGCCCT CATAGGCATTCCATAGATATTTGTTGAATGAATGCTTTTTCATATTGATTCCTACATTGATACA TTCTCAGGAGGACATTTGGCCTAT
WI-9720b	55 A G ---			---	CCTCTAACCAAGAAAAACTTGACTTCTCAACTCAAAATACCTTCTCTAATAATTTTJAGJAGTAACCA AAATATTCTCTCAAAATAAATTAATCTTTTAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CCACC

WI-9720a	47 A G ---	---	---	CCTCTAACAAAGAAACTTGACTTCCTCAACTCAAATACCCCTTCTCTAGJATAATTTAAGTAACCA AAATATTCCTTCAAATAAATAATCTTTTAATTAGAAAGAACACAGTGTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T ---	---	---	CACGCTCTAAGGCAGGATGGGCTATGAGATACTTTGCATTGTCTGTCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTACCTCTCTGTCTGTGATGAGATGAAGGCTCAGGGTGCTATJGAGGATTAG TAAGATCTCTTTCTAAGACAGGAGAGATTATTACAAGAAGAACTCACACAGGTTAGTTTGCAAT TAAGAAATGCCAGCTTTTGCTGTCATCATCTTGAACATTATCCACATG
WI-9748	74 C G ---	---	---	CCACTTCAGTAAATCAATTTGTAGCACCTTATTTCTAAAGATTCTAAATTTTATATGTTTACCCTTT GTCATTTCGTCAGACCAAGTACATGTTTTCACACAGCCATCTTCTTTTCCCTGGAATCTTTCAGAAT TACAGTTATGATGTCTCTTTTATATCCCCA
WI-9943	91 T C ---	---	---	TGAGGCTATGATTCAGATTGTGTAGTACTAATACTTATTAAGCAATTTCAATGTGTGGGCACTGTT CGTTGTGTTTATATCCATCTTCCTCTATTTTAAATTTCTACTGAGCAGAAAAAATAATGTATACATT AACCTTGTCTCCCTATTGTACCTTTTAAATTTGCAATTCACACCTTCTCTTTTGTCTATTTAGGGA
WI-9891	39 T C ---	---	---	AGGGGCTTCACAGATCCGTGAGCTCAACACTGCCTCTTCTGAGTGGCTGTGAACCCCAAGAC GGCTGGTCAATCAGTGTCACTCTCTCTTTCCGGACACTATCTTTAAAGAAAAAAGAGAGTGT CTTTGAATGATCCATTTATCCCCAAATAATCTTGTTTAAATAATCCCTTATAGGCCAAATCCAAAT GTGCTGAATAATCTGCCAAGCATGTCTTCTACACAAAAGGATTGCAAA
WI-9897b	84 C T ---	---	---	CTCAGAAATTAATCAGATCTTCCCCAAATGTCATGATCTTGTCTCAACATCCTATTTTCCCTCAAAC ATTTATCTAGCCTGTATJCAAGTCAATCCAGTGAGGCTGTTTATTTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83 A T ---	---	---	CTCAGAAATTAATCAGATCTTCCCCAAATGTCATGATCTTGTCTCAACATCCTATTTTCCCTCAAAC ATTTATCTAGCCTGTATJCAAGTCAATCCAGTGAGGCTGTTTATTTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115 C A ---	---	---	AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTGCACTJACCTCACAGAACTGGAAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGACTGGCAGGGGGAGTTCAGACA/CJAGCCAAGAAAAAGCC TGATATTAGAGGCACCTTGCAATTA
WI-9935a	42 C T ---	---	---	AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTGCACTJACCTCACAGAACTGGAAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGACTGGCAGGGGGAGTTCAGACAAGCAAGAAAAAGCC TGATATTAGAGGCACCTTGCAATTA
WI-9983	146 C T ---	---	---	CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCCTCCCATTTTCTTTGCTTGA TTCCCAAAACCCCAAGGTTCTCACCCAATCTGATCAAAATGCTAGTAGGTCTGCTGAGGTTAGGTTAA AGCATTATGA/CJTAGACACAAGACAAGAGAGTAAAGTTGCTGCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACATAAGTAAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A T A T C T	TGATGTAATGC TATGTAGCAA	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGTGAGTATACAGCAATCTATTTTGGTTATTTATGTGTGCTATAAAATCAATGGTTCTA ACATTTCAAATAGATCTTTTGGCTTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAAT CTA/ATTTCCCTAAGCACAGTAATCAAGGCCCTTCTACCCCA
WI-10020b	122	T A T T T	GCGAGAAAAG AAATCATGAC	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAAATTAATGTTAACTGGCTCTGAAAAGAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTATGGCGAGAAAAGAAATCATGACTTTT/TA/AAAAATACC AGACTAATGATTAAATAAAATTAACAGTCTAGGGTCCGGAAGTGGCCTAAAGCAGTAGTAGCCCT CCTTAGA
WI-10020a	39	T C A T A A A T T	TGTCATCTTGA CTCGTATTAA	AAATTCCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAAATTAATGTTAACTGGCTCTGAAAAGAATTTA GGCATGCATAGAGAAATAGCAGTGTTTTATGGCGAGAAAAGAAATCATGACTTTTAAAAATACC AGACTAATGATTAAATAAAATTAACAGTCTAGGGTCCGGAAGTGGCCTAAAGCAGTAGTAGCCCT CCTTAGA
WI-10064b	170	C T T T A C A T G	CCTTTAGATAT ATTGTGATTGT	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGAGGCATTATAATAAT ATAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGGTGACACTCTGTTTAAATCCAGTATCC CTACTCCTTAGATATATTGTGATTGTTTACATG/C/TTGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10064a	54	C A C A G G G A A G G	GTAGCAGGAT	GAGATGCTCTG CAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGG/C/AJATTATAATA AATATAATTGCAGAGCATCTCTCTCTATGCACCAGATATTGGTGACACTCTGTTTAAATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10289	29	T C C A A A C T C T T	TCTCTGTCCG	ATTCTTGTGT ATTGAATGGAA TTAA	CCAGGGATTCTCTGTCCCAAACTCTTAT/C/TTAAATTCATTCAATACAACAAGAAATTTATAGAA TATGCACCACATGCCACAAAGACACCCCTTATATTAGT
WI-1319	40	A T A T C T T T	TGGCACTTAG AACATAGTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATTCTTTT/TA/ACCATAGGGGTGTGGCTTATCT TTTACCTGGCATGGCTTAGGTCTGTTTATAATTTGGTATCTTTTGCCACAAAGAGTCTGTTCTGAC AGTCTTATGATCTCTAATTTAACATTAACACTGGTCAGATGTGTTTAAAACTTGTGAACCTGCAGC
WI-10316	104	T C C T C T T	CTGTTGATTT CTACCTCTATT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACCTTAGTGAGGTGTAATCAGAAAGCATCTATATTACCAGTCACCAACCCCTG GACTATAGTCTGTTGATTCTACCTCTATTCTCTTAT/C/TTAACTTTTGGATACATTCCCAAGCAT CATGGTCACTTCCAGTATGAAAGGATGTTTAAAGCCCAAGCC AGTGAGTTGTGCACAAATTTGGAGACATCTGTGACCCCACTTAAACACTTCTCCCAACA/C/TTAC AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA
WI-2572	61	C T ---	---	---	

WI-10368	31 C T	TGAAGCAACC	CAAGATATTAT	GAGGAAGCTGCCTGAAGCAACCAAGGCTGTGTTGCTACCCCTCTAGAGAATAAATAATATATCTT GAGATAGGGAGGAGCAGCCTGAGGACAGTCTGGGTTTTGTTCTACCCCACTGGGAAGCAGAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCCTGATGGATTGCCCTTTTCAGGG T
WI-10391	32 A G	ATGACTCCCA	GGGAGTTAGGA	CCTCCGTTCTCTGCTCAGGTATGACTCCCAJAGTCAACTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTTCCAGGGGACGCATCTGACACAGCCTTTTGTCTGCTGTGACAAACAGAACATTGCAGAAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A C	GCA	TGCCGCTTCCA	AGCGATGAAATTTATATGTTATGCTGACTTACGGGGTGCTCAATAAATAATTATTTCTTTTCATATT TTCCAATTTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAGCTTT CTAATAGCAAJACJAGCTACTGGAAGCGGCAAGAAATTTAAACCTT
WI-10567b	82 A C	---	---	AGCGATGAAATTTATATGTTATGCTGACTTACGGGGTGCTCAATAAATAATTATTTCTTTTCATATT TTCCAATTTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAG TCTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAAACCTT
WI-10567a	60 T C	CTTTT	GGTGCTCAAT	AGCGATGAAATTTATATGTTATGCTGACTTACGGGGTGCTCAATAAATAATTATTTCTTTT/CJTCAT ATTTTCCAATTTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAAACCTT
WI-11153b	84 C G	TACTTTA	AAATCCAACA	CGTTGGGAATTTCTATCTCACCTAAATATGCGTGATTAATAATACATTTTAAACAACTTCAAA TTGCTTTAAGTACTTTA/CJGJGAAGACCTTGACTGTGGATTTTGGAGTTTTTCTTTTATTTCTTAATA AAACATGCATATTTAAGTTGTGACGAAGATGACTTATGTTAATATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33 C A	AATTATG	GCAATTTGAAG	CGTTGGGAATTTCTATCTCACCTAAATATG/CJAGTGATTAATAATACATTTTAAACAACTTCTC AAATTTGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGGATTTTCTTTTATTTCTTAATA AAACATGCATATTTAAGTTGTGACGAAGATGACTTATGTTAATATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125 T C	ATCC	CCATGGCTGTA	GTTGTAAACTCCAGTATCATTTCCCTCAAAACCAGCTTAAATCACAATCACTTTTCTTTCTGTA GAGCTCAAACTCAGTCTGAATGAATTTGCTGCACAAATGTAACAAGAAATGATGATCTAT/CJACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C T	TGAGA	TTTGAGGTTTT	TGACTCAAAGGAAACACACAAAAAGTTTACCAGTGAATATGACCAAAATGAGJ/CJAAAT TTGTTAAAAAAAACCTCAATGAATGAAGAGACAAATATAGTTCAAAGATTCAGGTTCAATATTTGT ACCTACAAAATAGGGATAGTCATGGGTTTGGCAGACTTTCTTTCTTTCTTTTGT/GJCTCTTA GAATCCATTTTGTCTTTTGGCCAGCATTCCTCTCCCCATATTTTAAAGGAGAGAAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTCCCAATCCAGAGGAGGAGTACTATTACCCCATGGGGTCAT AGAGAGGATTAAACAGGGTGATGCCTGCAATGGGAATATTGAAAAACC
WI-10656	59 T G	---	---	



WI-11169b	154 T G TTTT	TTAACCAAGA GTTTTTCATTC	CTAACTTAAA ATCCTCATTC	CTAAGTGGCTGTTAGTGACCTTGAGTTAGATTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATTAAGCCTAAAGTAGTGCCTTTTAAACCAAGAGTTTTTCATCTTTTT TTTAAAAAAGAGCAGACATG/GJTATCATGTGTTCTGATAATTTTTTATATTTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95 A G TTGAAAA	AATAAGTGAA AGTAACTGAC	AAACTCTTGGT TAAAAAGCAC TACTT	CAGCATAGAGGCTGTTAGTGACCTTGAGTTAGATTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATTAAGCCTA/GJAAAGTAGTGCCTTTTAAACCAAGAGTTTTTCATCTTT TTTTTTAAAAAAGAGCAGACATTTTATCATGTGTTCTGATAATTTTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25 A G ---		---	CAAGTGCTTGGACCTTGGATAGGTC/A/G/ACCGGCTGAAGTTGGACAGTTGTTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTGTCTCTGCTAGAAATCTGAAATCTGATGCCCTGTCCAAGG[ AGAGATGGGAGACAGTCTCAATCTTGTCTAAATAATTCAAAATAGCCATGGGTTGGACAAAATAC AAGGTTAGTGCTCTCTAAGCTTTAATGGGCATA
WI-10686	133 C T AAGG	TGCCCTGTCC AAGG	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCTGTGGCACATAAGGCAAACTACTGAGCCCCATACAGAGTGTTTTATGTTAATATTATGAAA AAAGTCAAGAGAACAAAGATGATATAGTTCTGCTAGAAATCTGAAATCTGATGCCCTGTCCAAGG[ C/JTGTGCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAAGGG
WI-11175	77 T A A	AAATGATTCTT TCTGCTCAAG	CTGTTCTCACA TTCTTTTTGAA AA	GGTAGGATGATTCTAGATGCCACTTTACAGCCACTGAAATATATGCTCCCAATGATCTTTCTG CTCAAAAGAGT/A/JTTTTTTTAAAGTTATCTACTTATTAATTCGTCTTTTCAAAAAGAAATGTGAGA ACAGTACAAAATGTGTTTCAGTATAGCAAAATTAATAATTAATAAAGTAGAAAAAGAAAGCCCAATT TGGGC
WI-10694	144 A G TATGAGTTTC	TGCAAAATGCTT TATGAGTTTC	GGCATTTTGT AAGGAGGAAA	TAGAGAGGCTTTTCAGTTTCAGGTTGGAGGGTGGTGAGGTGAGATTCACTTCTTAGAAGCACTGGC TATGTACAGAAAGATAAACTCTGAGAGAACTCAGTTCTAAAGTTTCAGTCTTTGCAAAATGCTTTA TGAGTTTTC/A/G/JTTCTCCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGGCTTTCT T
WI-2716	23 T C C	TGAATTCATCC AGAAAAACAG	TCTCTTTTCTC TCTTGTGTCA TTC	GTGAATTCATCCAGAAAAACAGCT/C/GAATGACAACAAGAGAGAAAAAGAGAAATAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGCTCCAGTGCATGGAGCAGTG
WI-10719	115 T C GCCATTCTAG	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC	CAGGCCCAACTCTGTGCTAATTAAGTGTTTTAGAACAGACACCTCAGTCACACAAGTTCTCTTGTATGT GCCCCACATAAACAGTTACTGGAGGATGACTCTCAAGGCCATCTAGT/C/JGGCTGCTGGCAGTGCTT TTCAGCCTGCTGCCATAACTAA
WI-10721	40 A G CTTGCCA	TGGCTCTGCTA CTTGCCA	GAACTCCAC ATAAATAAT CTCA	CAACCAATTCAGATTTAATTTTTGGCTCTGCTACTTGCCAA/GJATGAGATTTATTTATGTGGGAGTT TCTGAAGATCCCATGGTAAATAGATTCTCTCTCCCTGCTTAGGTTTGAAGAAGTTGAA

WI-11204b	88 T C ---				GCACACGAAATTGATTAAATTGGCTGACCTTTGAGGAGGAGAACACAGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTTACCTTTT[C]ATTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTAATTGGGAAGAGATTTAGTGAATCAGAAAAAATAGCTGAGGAAATTTATTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAAGGG TGAAAAAGAAA TACCTTT	TGATCAGCTTAA AATGTACATAA		GCACACGAAATTGATTAAATTGGCTGACCTTTGAGGAGGAGAACACAGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTTT[A]CACCTTTTATTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTAATTGGGAAGAGATTTAGTGAATCAGAAAAAATAGCTGAGGAAATTTATTCAGAAG GCAACATC
WI-10732	80 C A ATTGGTCACT	GCTGTGCTTC ATTGGTCACT	AAGAACAAATG CATAACAGAA CTTTAA		ACATGTAATTCCTTTAGTGGTCAGCCTTCCTTACCCCAAGAATATCCCTGGTTTATGCTGTGCTTC ATTGGTCACTT[C]ATTAAAGTCTGTTATGCAATGTTCTTGAGTCCACATAGGTGTTAATCATTTCCA CACCACCTCTGTTTAACTGTC
WI-11206	127 A T ACTC	GGTGTGTTTT CTGTATGTACA		GAGTGACAATC CTAATGGTTGG	TAGTCTTTTCTTTGTACGAGTGTCAATAAAGAAATACCACCTGTCACATTTTGTAAAAGATAGCACAG AGAGAAAGCATTACAGGGCACAGCACAAACATGAGGTGTGTTTCTGTATGTACAACTC[A]TCCAA CCATTAGGATTGTCACCTCATATATAGACAGAATTCAGTGGTGGTGAATTTGAAATTCACACACATGGA ATAAGTCTA
WI-11215	68 C T ---			---	GAAAAAAGTTTTAATTGGATTGCTTAGTTTGTCTTAAATTTGACCTACTTTCAGATTTATTTTAGT [C/T]ATTTTCTATAATATTTCTTGAAGTGATGGATTTCTATAAATTAAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTTATCCAAAGCCCCCATTCACCATGT TTT
WI-11219b	89 G A AGAGAAA	GAGAGAATAT TCCAAAAAGT			ATGAAAAATGCATTAGAAAGATTGGAGGATAAAATTGAGAGAATATCCAAAAAGTAGAGAAAAA GAGACAAAGAGATGAAAAATAGGA[G/A]AGAAAGTGTAGAAAAATTAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAAATGAAGGGAGAAAAATCCAC AAAAATCTC
WI-11219a	18 G A ---			---	ATGAAAAATGCATTAGAA[G/A]AATTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAAATGAAGGGAGAAAAATCCAC AAAAATCTC
WI-11222b	136 G A GGCTGG	CATACCACTGC AGTTGTGA			AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAAATGCTAAAAATTGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCACCCTTGAACATTTGTTAAACATTTACAGCATACCCTGCGGCTG G[G/A]TCACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTTGCTTTCACAGGCTACTGG AAAGCC

WI-11222a	25	C T A	GCCACAGTGG AATCATTTAG	TTTAGCATTT GCTGATTCG	AGCCACAGTGGAAATCATTTACACTA/C/TJCGAAATCAGCAAATGCTAAAATGGGGCTTTGGATTTT TGTTTTGTTTTTTCATAGACCCACCGTTGAACATATTGTTAAACATTTACCAGCATACCACCTGCGG CTGGGTCAACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTTTCACAGGCTACTGGA AAGCC
WI-10775	39	C T CACTC	TTTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTTTTATGCCATATTAATTCATTACACTC/C/TJACATCATATTTCTTAGCAAAATACA TCTAGACACCTGGCACTCAGTAAGGATATTCCTGGCAGATAATCATTTGTTATCATTTAGACATTGCA GGAACCAACCATATGGATGGATAAATGTGTGTTTAAATGAAGGCAAGCAATTA
WI-11226	165	A C ---		---	TTGCATGCATTTATACGAAAGGAATTAATAATATCTTCTTATAGTTGAATTTTAAAGTAAAAATAAA GTTTACATATAATACAAAAAGTTGTAAGTATAGTAACAATGAATTAGAAAAATGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA/A/CJGACATAGTTGCTAAGGATATTCACACAAATAT TTCATGA
WI-10778	62	A G G	GCAAGGGAGG AACATTTACA	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGCTACTGACAAAACGTAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG/A/GJG TCCATCTCTGATGTCACCGAGCGGCCAGGAAGGTTGATCTGGAG
WI-10789	21	C T GCTCTAGACC	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGGA	TGGGACACACTGCTCTAGACC/C/TJCCCAGGGTCCCTCAAAGGTGGGTGTAGAGGCCCTACTGCCCT GCCCTGGGACGACAGGACATCAGGGCCTTAGTCTCTGGGACAGTGAAGGGGCCACCAAC
WI-10810	58	C T GCAGGAATT	CATCTTCATGG GCAGGAATT	CAAAACCCTAAG AAACACAGAA ATG	ACAGAAAAATGCCTAGTCTTGTAGCAAGAGAGGAAGCATCTTCATGGCAGGAATTC/TJCATTT CTGTGTTCTTAGGGTTGTGGCTGGCATCAGTTCACATCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCCCTCTAGAAGTCATGCAAGAGAAAATGATGA
WI-10828	23	T C ---		---	GGACCAACACAGAAATTTACTTGGCAT/CJAGGGTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAAGGCTATAATATTGGATACATTAGGCTCATTATGAATCTCAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10832	91	G C AGGCTCTCC	CATTAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	TATGCCTTCCCAACGAGCCATCCACGCTGCTTAGCACAAAAAATAGATACATCATCTGAATG GGCACATTAATCTGCAGGCTCTC/CJTTTCTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGGAGGAGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGTTCCG
WI-10834	96	C T GTGTTAAT	AGAATTAAC GTTCAAAAGT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTATCAAAATTTGCCCAAAGACCAATTAAACAAGATTTAATAGTTAAAGCCAAAACATA AAGAAATTAACGTTCAAAAGTGTGTTAAT/C/TJCTTAATACCAATTTTATAGGGCCACCAATTAACCT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24	T C ---		---	GGATGATGTTCTGTGGTCCCTTAT/CJAAAGCCCTCTTGATCCCCAAATGTGTAAATTTATTTATCT TGGTATTTCTCGCTTACCCATAGTCACCTGTCAAGTGTTCCACCCCT

WI-2296	81 A	G A	TGTTACTTTGA TTCTTTGCTGT	GCAAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCTAGAAAGGTCTCAGGCTTTAGAATAAGTTGTTACTTTGA TTCTTTGCTCTGAC[A/G]CCAGTTAGCTGTGATTTGCAGAAGGTTACATTTGTTTGTG
WI-2300	77 G	T C	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTTCATCATGCTGCTTCCCTGGAAATTTCCCTTTATTTGAGCGGGGCGAGGTGGTAGGCACAGAAGC CAGTCATAC[G/T]TGCITTTAAATTTGACCCCAACCATTTACTAAGAAATAGCATTTCA
WI-2371	55 G	T C	GTCCTGTTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAGGTCGGTCTTCTCCAGCTTCT[G/T]GTGGTGGCT GTCAATCTTTGACATTCCTGTCTTGCAGCTGTATAATCCATCCCTTGCCCTCCAGCTTTACATGATGT TCTCTCCGTGTGTGTG
WI-2395	122 A	C	GAACATATTT GTAGAAAAT	TCACCTTTCTA TTTATTCTGAA	GGGGGCACAATTTAGCTACAGTGCATATTTAAAGATAACATAGAAATATCATATAACTTGGTTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTTACTATCCAA[A/C]CTGAATTC AGAAATAATAGAAAGGTGAATCATCTTATATCATTAAAGAAAGCTAAATTTATTAGTAACAATCTTTA CATTTACACAACCCCA
WI-2437c	192 G	A ---		---	CACCAGCCACCACCTTACAACTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179 G	A ---		---	CACCAGCCACCACCTTACAACTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128 G	A ---		---	CACCAGCCACCACCTTACAACTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA TAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71 G	A TTTTAGTT	GCAACCTACT GACAAATTTAA	AACAACCTGTC TATTGGTCTCA	CAGTAGGAAACGGGTCTTCTCCTTAGACCCCTCCAGAAAAATAATGCAACCTACTGACAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCGAGAACT
WI-1356	123 T	C GAAAA	TGTTTAGGAA ATAATGACAA	TGGTTACAAC GTACCAAAACAT	CTGTAACCTACACACATCCTCCTGTAACTTAGGTTACTTGTATACAAAAACACAATGTAAATGCT ACATAAAATAATTGTACATATATTGTTTAGGAAATAATGACAGAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCCAGCCATTTTCCCCCAATAATTTCAATCCACAGTTGGTTTAAATCCACAG AAACCACGAATG
WI-2886	46 C	A GGGAGAAGA	CAGAGTCTGG	TTGCCATGCTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAAGA[C/A]AACGAGATAAAGCATG GCAAGACCACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACATTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTCAGAAGAAACAGAGGAGCGTT

WI-2906b	77 T A	---	---	CCTGAACACCTGGAGCAGCTCCCTCCCTGGACACCTTCATCTGCTGGAACCTTTCCTGGAATGCTC TTTCCCTCT/AJGAGCTTTGCTGGCTTACTTTTCTTTTCTTTAGGTTTCAGCTTCAAAGTGACCT CCTAGAGTTGGTTTGGTACCAACAAA
WI-2906a	50 A C	GACACCTTCAT TCTTCTGG	AGAGCATTCCA GGCAAGT	CCTGAACACCTGGAGCAGCTCCCTCCCTGGACACCTTCATCTGCTGG/AJGACJTTCCTGGAAT GCTCTTTCCCTCTGAGCTTTGCTGGCTTACTTTTCTTTTCTTTAGGTTTCAGCTTCAAAGTGACCT CCTAGAGTTGGTTTGGTACCAACAAA
WI-1736	175 C T	---	---	TACTCCTCATTCTCATGTCCCTAGACGCTACTCAGATTTCCATGCCCTGAAACATTTATTTCCCTAAAT TAGATTTCCACCCCGACACTATTTACACAGAAACAGCATGGAGCAGTTTGGAGTCTGGCTCTTAGA GAACCTACTTAAGGACAGTGGTTTCCATCTGCTTCCA/CJTJAGAGATCTAGGGTGTCTTTGGAACC ACCTTGG
WI-1851	136 G A	GCATTGAATT AACTATAGAT GTGTTAAGTA	CAC TAGCAATG TTAACTGAAG TTG	AATACCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTTAACATATTAATCTGGGGAGG ACACAAACATTTAGACCATAGCATTTGAATTAACATATAGATGTGTTAAGTAATTTATTAACATGGTA CA/G/AJACAACCTCAGTTTAACTTGCTAGTGATTCATGTTGATACCATGTACCTTCTTACATCATG TGA
WI-3000	62 G A	CCCAAAACAC AGAGACCCG	GCCACTATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCAGCTGTCTTACATCTCTAAATGTGAGCACCACCAACACAGAGACCCCTG/AJT GAGTCTTAGTCAATCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT
WI-1754	177 G A	TTTTCTCCCTT CTTAAAGAGA TAGTC	AAAGTCGAATT GCTCTGG	ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACT TAAGGGTTAGCAAATTCACCTGACAAAGAGTTAGGTTTCAACATTTGACCTCATAAAGTGATTTT TTCTCTTCTGTTTGTCTTCTCCCTTCTTAAAGAGATAGTC/G/AJCCAGAGGCAATTCGACTTCTGT AGCCACAAGATT
WI-3167	37 T A	AAATCAACC ACAGATCTAT TAGATTTC	TGTGATAGTTT TGAGATGGTG	ACAACACAGCAAATCAACCACAGATCTATTAGATTCT/AJACCCCATCTCAAAACTATCACATCAA AGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140 G A	GTGGAGTGGGC AGATAAAGA	TCACTCAAAC AGGCTTGG	CAAGCACACATTCAGGCAGTGGGCAGGTAGGGAAGGTGGGCAACTTGGCAGCAGAGAGAGGGAAG AAGTTCAGACCGTTGGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGCGAGGTGGTGGAGTGGCAG ATAAAGA/G/AJCCAAGCCCTAGTTTGAGTGCACACTGTGGGATTCAAG
WI-1775	47 C T	CCTGCATGGTC TTTTCTCTG	AGTTGAGATT ATGACAATGAT GTAA	ACTCCACCAACAGTTTTGTGAGCCAAACCCCTGCATGGTCTTTTCTCTG/CJTJTTACATCATTTGTCATA AATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55 G A	AGCATATTCA TTGATTTCCCT ACAT	GAGGACTTAAA AAGGAGCAATT G	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCATTGATTTCCCTTACAT/G/AJCAAATGCTC CTTTTTAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAATAGATTTCCCTTAGGA

WI-3416	33 C T	CCAAGTTGTA GCATTGAGAA	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCCTCCAAGTTGTAGCATTAGGAGTCTCTCTAGAGGTAGTTGTGCTGCGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTACATCTCTCCAAACAAGTGTACCAACAGCATTTGTTAAG GAAATGTGCAATGCTTGCTACCTCTGACGACACAAATTAATCCCATTTGCTTAAAAAGACACAGG
WI-3453	70 C T	TTCTTAGGCCC ATCAGAGAA	TCAATTTCCC CATGACTTC	TCCTATTCTTACAACAACAGAAATTAACAAATTGAAATCAGCTACTCTCTTAGGCCCATCAGAG AATCTGAAAGTCATGGGAAATTTGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109 GA	---	---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACCTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTATTTAATGAGGTGGTGGAGAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90 A G	AGTCAGTTTCC CTAATTTTAGC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACCTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTATTTAATGAGGTGGTGGAGAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3502	79 C T	CCTGGGTTTCT GGATGTCT	GGGTGACCTG TCCTCA	TTTGACCCCATACATGAGAAATAAACCATAGAAATGTGGAAAAATAAACGGGAGAGACCTGGG TTTCTGGATGTCTCTTTGAGGACAGGGTCAACCCAC
WI-3600b	146 G C	GGTTCTAACC TGGATATAAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTGACTCTGCTGCTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTGCTTCCCTGCTTAAAGTTATCCAGAGGTGGTTTCTAACCTGGATA TAAACATCTGCTATGGAAGGCTGCACCTGGATGAGGTCACAAA
WI-3600a	78 T G	CCATGCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTGACTCTGCTGCTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTGCTTCCCTGCTTAAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTCACAAA
WI-3678	125 GT	---	---	TAAATCATGCTTATTTTACAAGGTAATCCACTCACATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAGCTCTCATGCTCTTCCCTGAACCTTCTACTTACTGTGCTGTTATGATGCACTGTTCTTTTGG ATAGATGGTTGATAGGAGATGGGTTGTTAAAGACACAATTTACCTTGTGTTTTCAGGCAGAAATAG ACTCTCTGTGTAAATCACTGAATGAGTTCCTGCTTATGCTTAC
WI-3687	67 A C	---	---	AAAGCGATGTTGAGATACCACATTCATGAAAGTAAACACACACACACAAAAATATGACATAAAA TIA/CJAAAACTACTATAGTTTATGAAATGACTTCCAAAAATTCAGAGAAAAAGTCACTTAAACAGG ATTCTCAATTCAATCCAGAAATCTCTCTGCTTAACTTTGACTGCACAG
WI-3735	72 T C	CCTCAGTTATG TATCAAAATGA	GGCTCACCAT CATTGTTTT	TCTAAATGTGAAACCAAGAAATCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAACIT/CJACACCGGTTCAATGAAAAAACAAATGATGGTGAGCCATGTCCCTTATTTAATGAAAA GATCTGGGCAATTAACCTG

WI-1819	51	C T	---			<p>GA AAAAGCAGGAAGCCAGGCAGGACAAAAC TTTTGAAAAAGTCTTTT CAGCAC/C/TTTCGTGGATCCG</p> <p>AA TTTTAGTGTGATTTGGCAGGCAATGCGGGTAACATGTTCCAGTGTTTTAACTTGCACAGAA TTGC</p> <p>CAGATTAGCGATTGTTTGACTTGTCCAATTAATGAAATGTGGAAAAA AAAAAAGGGTGGTAACTGTT</p> <p>AAGCCTGCTGCAATGTTTAGACAGAGGGTGGGGTGGGAGGTGGAATACC</p> <p>GGCCTATTACATGACACTGGGCCAAGATCTTGCTCCCTTTCTTTCAATAGATAGACTAACTAGAAA</p> <p>ACTGCCCTGGCCCGAAGATGGTTGTCTTCATCATCTCTGCTCTG/C/G/AGGCCCCAGGATAAAGCA</p> <p>GGCA</p> <p>AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCTGACAA/T/C/CGGATGTACCTAGT</p> <p>ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAGACACAGT</p> <p>CATTAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG</p> <p>CATC</p> <p>CAATGACCAATGTCTTTAGAAAGCAG/AC/CGGAGAGGACACCCGACGAGACACACAGGAAGGAGTGAG</p> <p>GTGAAGATGAAGCAGTGTGACGCAGCCACAAAGGTGAGGAAGAGCAAGGGTGTCTGGCCACT</p> <p>GGACCATTTGTCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCTTAACACTGTGAOCTCAGGCA</p> <p>AGTCATGTCTGCTTCCTGAACCTCGGCTTCCTCACCTGACAAGTGG/AG/TATCATGTGTCTACACTGC</p> <p>AGTGTTTATAATGCTGCAT</p> <p>CTGAGGAGATTGATGCTACTTTACCTGAGGAAAC TTTTATTACCTCCCTGAGTTTGTTCCTTGCAA</p> <p>GACATTGCTGATTCTCTCAAGACTCACAGC/C/TAACCATCTTCTGCTTAGACCTATAACTAG</p> <p>ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA</p> <p>CAAAAGAG</p> <p>CCACTCCCAGGCCAAGAGCGTCTATGAATCAT/G/ACATTTGTTCTGTTATTGCTGTTACACAGAGT</p> <p>GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC</p> <p>TAATTACATTGCTCTGTTTGTGCAATTTATGCTCTCTTATGTAACAACAATCACCAACACATTGAGG</p> <p>TC TTAGTCATTGCATG/AT/JTGATAACAATATGTCACTTAATAGGAAC TCAAGCATAGTTATGTT</p> <p>ACATTTATTGCTAACAGCAG</p> <p>TCCTCTCTGTAATAGGAAGTCTGATTAGATGCC TTTTGAGGTAGGTGGCTCTAAGATGGTAATT</p> <p>ATCTGTCCAAGTTTGTTCCTATAATTTAGCAACAATATCAACAGAA/AG/GGGCTATATTAGAAA</p> <p>ATTCTAOCCTGCATCCOCCCTGGATCTGAACGTTCTTCATGATACT</p>
WI-3746	116	G A	---			<p>AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCTGACAA/T/C/CGGATGTACCTAGT</p> <p>ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAGACACAGT</p> <p>CATTAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG</p> <p>CATC</p> <p>CAATGACCAATGTCTTTAGAAAGCAG/AC/CGGAGAGGACACCCGACGAGACACACAGGAAGGAGTGAG</p> <p>GTGAAGATGAAGCAGTGTGACGCAGCCACAAAGGTGAGGAAGAGCAAGGGTGTCTGGCCACT</p> <p>GGACCATTTGTCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCTTAACACTGTGAOCTCAGGCA</p> <p>AGTCATGTCTGCTTCCTGAACCTCGGCTTCCTCACCTGACAAGTGG/AG/TATCATGTGTCTACACTGC</p> <p>AGTGTTTATAATGCTGCAT</p> <p>CTGAGGAGATTGATGCTACTTTACCTGAGGAAAC TTTTATTACCTCCCTGAGTTTGTTCCTTGCAA</p> <p>GACATTGCTGATTCTCTCAAGACTCACAGC/C/TAACCATCTTCTGCTTAGACCTATAACTAG</p> <p>ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA</p> <p>CAAAAGAG</p> <p>CCACTCCCAGGCCAAGAGCGTCTATGAATCAT/G/ACATTTGTTCTGTTATTGCTGTTACACAGAGT</p> <p>GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC</p> <p>TAATTACATTGCTCTGTTTGTGCAATTTATGCTCTCTTATGTAACAACAATCACCAACACATTGAGG</p> <p>TC TTAGTCATTGCATG/AT/JTGATAACAATATGTCACTTAATAGGAAC TCAAGCATAGTTATGTT</p> <p>ACATTTATTGCTAACAGCAG</p> <p>TCCTCTCTGTAATAGGAAGTCTGATTAGATGCC TTTTGAGGTAGGTGGCTCTAAGATGGTAATT</p> <p>ATCTGTCCAAGTTTGTTCCTATAATTTAGCAACAATATCAACAGAA/AG/GGGCTATATTAGAAA</p> <p>ATTCTAOCCTGCATCCOCCCTGGATCTGAACGTTCTTCATGATACT</p>
WI-3867	49	T C	CA A			<p>AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCTGACAA/T/C/CGGATGTACCTAGT</p> <p>ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAGACACAGT</p> <p>CATTAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG</p> <p>CATC</p> <p>CAATGACCAATGTCTTTAGAAAGCAG/AC/CGGAGAGGACACCCGACGAGACACACAGGAAGGAGTGAG</p> <p>GTGAAGATGAAGCAGTGTGACGCAGCCACAAAGGTGAGGAAGAGCAAGGGTGTCTGGCCACT</p> <p>GGACCATTTGTCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCTTAACACTGTGAOCTCAGGCA</p> <p>AGTCATGTCTGCTTCCTGAACCTCGGCTTCCTCACCTGACAAGTGG/AG/TATCATGTGTCTACACTGC</p> <p>AGTGTTTATAATGCTGCAT</p> <p>CTGAGGAGATTGATGCTACTTTACCTGAGGAAAC TTTTATTACCTCCCTGAGTTTGTTCCTTGCAA</p> <p>GACATTGCTGATTCTCTCAAGACTCACAGC/C/TAACCATCTTCTGCTTAGACCTATAACTAG</p> <p>ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA</p> <p>CAAAAGAG</p> <p>CCACTCCCAGGCCAAGAGCGTCTATGAATCAT/G/ACATTTGTTCTGTTATTGCTGTTACACAGAGT</p> <p>GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC</p> <p>TAATTACATTGCTCTGTTTGTGCAATTTATGCTCTCTTATGTAACAACAATCACCAACACATTGAGG</p> <p>TC TTAGTCATTGCATG/AT/JTGATAACAATATGTCACTTAATAGGAAC TCAAGCATAGTTATGTT</p> <p>ACATTTATTGCTAACAGCAG</p> <p>TCCTCTCTGTAATAGGAAGTCTGATTAGATGCC TTTTGAGGTAGGTGGCTCTAAGATGGTAATT</p> <p>ATCTGTCCAAGTTTGTTCCTATAATTTAGCAACAATATCAACAGAA/AG/GGGCTATATTAGAAA</p> <p>ATTCTAOCCTGCATCCOCCCTGGATCTGAACGTTCTTCATGATACT</p>
WI-3898	25	A C	G			<p>AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCTGACAA/T/C/CGGATGTACCTAGT</p> <p>ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAGACACAGT</p> <p>CATTAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG</p> <p>CATC</p> <p>CAATGACCAATGTCTTTAGAAAGCAG/AC/CGGAGAGGACACCCGACGAGACACACAGGAAGGAGTGAG</p> <p>GTGAAGATGAAGCAGTGTGACGCAGCCACAAAGGTGAGGAAGAGCAAGGGTGTCTGGCCACT</p> <p>GGACCATTTGTCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCTTAACACTGTGAOCTCAGGCA</p> <p>AGTCATGTCTGCTTCCTGAACCTCGGCTTCCTCACCTGACAAGTGG/AG/TATCATGTGTCTACACTGC</p> <p>AGTGTTTATAATGCTGCAT</p> <p>CTGAGGAGATTGATGCTACTTTACCTGAGGAAAC TTTTATTACCTCCCTGAGTTTGTTCCTTGCAA</p> <p>GACATTGCTGATTCTCTCAAGACTCACAGC/C/TAACCATCTTCTGCTTAGACCTATAACTAG</p> <p>ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA</p> <p>CAAAAGAG</p> <p>CCACTCCCAGGCCAAGAGCGTCTATGAATCAT/G/ACATTTGTTCTGTTATTGCTGTTACACAGAGT</p> <p>GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC</p> <p>TAATTACATTGCTCTGTTTGTGCAATTTATGCTCTCTTATGTAACAACAATCACCAACACATTGAGG</p> <p>TC TTAGTCATTGCATG/AT/JTGATAACAATATGTCACTTAATAGGAAC TCAAGCATAGTTATGTT</p> <p>ACATTTATTGCTAACAGCAG</p> <p>TCCTCTCTGTAATAGGAAGTCTGATTAGATGCC TTTTGAGGTAGGTGGCTCTAAGATGGTAATT</p> <p>ATCTGTCCAAGTTTGTTCCTATAATTTAGCAACAATATCAACAGAA/AG/GGGCTATATTAGAAA</p> <p>ATTCTAOCCTGCATCCOCCCTGGATCTGAACGTTCTTCATGATACT</p>
WI-3901	114	A G	---			<p>AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCTGACAA/T/C/CGGATGTACCTAGT</p> <p>ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAGACACAGT</p> <p>CATTAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG</p> <p>CATC</p> <p>CAATGACCAATGTCTTTAGAAAGCAG/AC/CGGAGAGGACACCCGACGAGACACACAGGAAGGAGTGAG</p> <p>GTGAAGATGAAGCAGTGTGACGCAGCCACAAAGGTGAGGAAGAGCAAGGGTGTCTGGCCACT</p> <p>GGACCATTTGTCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCTTAACACTGTGAOCTCAGGCA</p> <p>AGTCATGTCTGCTTCCTGAACCTCGGCTTCCTCACCTGACAAGTGG/AG/TATCATGTGTCTACACTGC</p> <p>AGTGTTTATAATGCTGCAT</p> <p>CTGAGGAGATTGATGCTACTTTACCTGAGGAAAC TTTTATTACCTCCCTGAGTTTGTTCCTTGCAA</p> <p>GACATTGCTGATTCTCTCAAGACTCACAGC/C/TAACCATCTTCTGCTTAGACCTATAACTAG</p> <p>ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA</p> <p>CAAAAGAG</p> <p>CCACTCCCAGGCCAAGAGCGTCTATGAATCAT/G/ACATTTGTTCTGTTATTGCTGTTACACAGAGT</p> <p>GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC</p> <p>TAATTACATTGCTCTGTTTGTGCAATTTATGCTCTCTTATGTAACAACAATCACCAACACATTGAGG</p> <p>TC TTAGTCATTGCATG/AT/JTGATAACAATATGTCACTTAATAGGAAC TCAAGCATAGTTATGTT</p> <p>ACATTTATTGCTAACAGCAG</p> <p>TCCTCTCTGTAATAGGAAGTCTGATTAGATGCC TTTTGAGGTAGGTGGCTCTAAGATGGTAATT</p> <p>ATCTGTCCAAGTTTGTTCCTATAATTTAGCAACAATATCAACAGAA/AG/GGGCTATATTAGAAA</p> <p>ATT</p>





WI-5204	54 C T ...		...	TAGATTTGATTGATGACATAGGGAAGCCTTTGTAAATTTGGGTTTTGAAGAA[C/T]GAAGAAAA TGGAAAGGAAGAATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAAATCCAGTTTGACTGGA ATATAGAGTGATGTACAGGGTGTG
WI-5215	70 A G C T C A A A A A	GGACCTTAAT ATTTAACAGA	AGATAATTTTG TAAAGATAGTT TTGGC	TTTTCCCTTATTTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[G/G]CGCAAAACTATCTTTACAAAATTTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112 T G A T A T A A	TTGTATCAAA GAGATGGGT	AATTAAGAA ATCTTTACATG GTTCITT	CCCTGAATGTCTTTGCTTCTCTCCCACTCTCTAGGGAACCTTTTCCATGTGAGGTGAAGGTTTGA AGAGTACTTTAATTAACTTGATCAAAAGAGATGGGGTATATAAT[G/J]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGTCTATCAGTAAA
WI-4456	49 C T T A T A G T T C C	AGTTGAATTA TTCAGAAAAT	TTTCCTGTAT GCATGAACITG	ACACATTTTCATTTTGCCTTAAAGTTGAATTATTCAGAAAAATTATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCAAGGTGGGCAATTGATTGAATTGT
WI-4461	49 A G C C T T C C	TCACTGTTATT TTAAAATTAT	TTTGACCTTC ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAATTTATCCTTCC[A/G]TGAATTTGGTGAAA GGTCAAGAATGAATCCACCTTTAGATTTCTGGAAATTTTATTTGGATGATAATGCAATGGGC CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGTATATAAAGAAACACAGTTAGTAATCTT TCACCTTT[G/A]TATTTCTCTCTACCTCAGGGAATC
WI-4465a	41 A G A C A C G A A A G T	AAGCCAGACA ACACGAAAAT	GGTGAAGATT ACTAACTGTTT TCTTT	CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGT[G/J]TATAAAGAAACAGTTAGTAAT CTTTCACCTTTGATTTCTCTTCTACCTCAGGGAATC
WI-1949b	160 T C T A A T C	GAGTGAATAA ATGAATGCCA	TGAGAGGTGGG GACAAAA	GGGGTTAGGACCTCGAGATCTTTTCAAGAAAGCACAATTCAAACCATTAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/J]CAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAATAA GGAGTGAATAAATGAATGCCATAATC[T/C]CTGTGTTTTTTGTCCCACTCTCAGACCTTTCCCTGG CACA
WI-1949a	86 T G A T G C T C T G A G T	CAGTGGTGAG ATGCTCTGAGT	CCATGTCAGCA GCTTG	GGGGTTAGGACCTCGAGATCTTTTCAAGAAAGCACAATTCAAACCATTAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/J]CAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGTCCCACTCTCAGACCTTTCCCTGG CACA
WI-4529	64 T C A A G A T G	CCAAGTAAGT CTATCAATCTG	TTCTAAAAATA ACACTTCCTGA AAAA	TGAGAGAGTTTTGGATTATTCATCCTCTGCAACACTCCCAAGTAAGTCTATCATTTCTGAAGATG[T/C] GAGTTCTCTTTATATCCTATGATTATTTTTCAGGAAGTGTATTTTGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATCCGCTGGACAAGATGGGCCCTAGGATCATTTT

WI-4540	110	A G C A T C C	GCACCATGTGG C A T C C	GACAATGCAGC C A T G C A	AGCTTTTCCTTTCTTAAAAATTTGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCC[A/G]TGATGGCTGCATTGTCCAGTC AAATGAGACAACCTTCCTAT
WI-4582	226	T C ---	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAATACCAACAAACACCCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATCAAGGCCAGTTTAACTTATTCCTGTACACA AATACTTTATGGGAGACAGCATTTAATTCAAATCAATAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTT/CJCCTCCTTGCTAGAAACCATTTGAT
WI-1965	105	G C A G	GCCATTGAGG AAGTGTTAA	GAATGGATGGG T C A T C T C T	CAAAGGTTAGTTTAACCTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGCCATTGAGGAAGTTTAAAG[G/C]JAGAGAGATGACCCATCCATTCTCTGG GCTTCTTATATGACACCATACTATCCACACAGATGTGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99	C T T T G	CACTGTTTCT ATTGACCGTAC	AGAAAAGAG AAGAAGGAA A A A	TGTTTAAACCATACAGTTTGTGCTGCTACGTTGTTAGAGCAACCCAGAAAATTAACACGCCCTAG CATTTTCACTGTTTCTATTGACCGTACTTG[C/T]CTTTGCTTTTTTCCCTTCTCTCTTTTCTG CCCTCTTTTAACATA
WI-5248a	38	G C T A C G T T G T	AGTTTGCTG CTACGTTGT	TTTTAATTTT TGGGGTTGCT	TGTTTAAACCATACAGTTTGTGCTGCTACGTTGTTAG[C/J]AGCAACCCAGAAAATTAACACGCC TACCATTTTCACTGTTTCTATTGACCGTACTGCTCTTTGCTTTTTTCCCTTCTCTCTTTTCTG CCCTCTTTTAACATA
WI-4596	69	T A A G C A C T G T G A	TGAAGCAGAA AGCACGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTCTCGGTGACATTACTCTGTTGACTTTGCTGTAAGCAGAAAGCACTGTGA CT[A/C]ATTATTAGGCCATCTCCTGCCTGAAGCCTGCCTACAGCAATTTGTAAACATATGGCATTTGGG ACATACTCTGAGCCCATCACTATTGACAAGATTCTCCTTTTAAACA
WI-5252	119	A C ---	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAACTCTGGGAAAGGATTTGTGATGATCATTTG AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTTGCTTT[A/C]TACCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61	A G C T	GCAATGCTAG AAAATTATGC	TTAGGTGCTTA AGTTGCTACT TGG	TGCAAAAAGGAAAATGATAACCCAGGACTGTTGTTCAAGCAATGCTAGAAAATTTATGCCTA[A/G]C CAAGTAGACAACCTTAAGCACCTAAGGCAGAAATGAAAGTTTCTCTGTGCTATTAGTCCCTCTATTCA ATTACCATTTATCGGGTAATTAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGCTTTTGCTATGCT
WI-5257	77	C A G C A A A G A G G	GAGGCATGAA TGAAAG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATGGGGCAAAATTAAGCATATGAAAATACCAAGTTTGGCAGAGGCATG AAGCAAGAGG[C/A]CTTTCATCTGCCCTGGTGGTTTTTTCAGTAAGTCAACATGTCTTTGCCCTCC CGGATGAAAGATACCCCTTCTATGACTCAGCAATCCACTCCTAGGTATGCACCCCTAAACATGGGTG GCAAAAT
WI-4649	50	C T T T C C G A A T G	GAGACCATCT TTCCGAATG	TGTAAGGTG TACTTACAAGA AATCATC	TCAGTGTTTAGAAAATTTCTTCTCCTCAGTGAGACCATCTTTCCGAATG[C/T]GATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGTCTACCTGAATTTGTATTTTTTAA AAAATCCTCCCAATATG

WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT G	CTGAAGTGTTA AACTGGATTG G	AACTGTGGTATGTATGTTGTGTTTCTGGAGAGTCAGTTACTCTCACTAGATCAATAAAGGG GACTTGGGAACCAAGATATCTAAGACATTTAATCCTAGAAGCACAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTAACACTTCAGTAACGTT
WI-4677	82	T	C	TCCAAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTCGACATTTTGGAAAAAATTGTCCAAAAGTGATTAGGTGAAAAAT GAGTTGAAATAAATG[T/C]AAGTTGAATAATGACACTGTTGAAAAATGATGAATCTGCTTCAATTCA CATGGAAGGAGACTAGAACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGCTATCATGAGGAATCTGTAGAAAAATTTTCCCTGGCAATGATTCAATAAAGTTTGTCC TCACCTGGGAACCTGTTATCTGTGATGTCAGTGACATTTCTTTTGTGACGGAAGAAAACTTCAA C/GTTTCGAGAAGGCTTAGATTATATCGCTGAAGCCCATCTG
WI-4722	88	G	A	TGCATATGG AACACCACAC G	AATATGGAATC TGCATTGAGTT G	CTTCCCATTTCTGCCAGTTAGATGACTGCTCTCCACCAGCTAGAAAAAGATGGGAGATTATTTTC TGCACATATGGAACACCACAC[G/A]CAACTGAATGCAGATTCATATGAACTACTGGGAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCACCTTTGATGGTTGAGATTTTCAAGAAACGTGAAATTTATGAGTAACCATGGG TCAACTATGAT[C/A]CCAAAACAGCAGTGTGTCTTAAAAAATATGATAGTTTCTTCTCCTGTCCACC GCAATGAAAAGGAGTT
WI-2028	176	T	C	TGTTACGTTT CCTGTCTCATC GAA	GGTTGGAACCT CAAATTACCTA GAA	GACTACAGCGCACAGACAGGCATTGTGTGGCTTGCACAGGTTTGGTTTGTGTTTAAAGTTAGATT TGAATCCTTTTAAAGAAAGAAAGTGCTCTTCAAGTTTACTACAGACCTCATCATCTCCTGGTTCTCTTG CACCAGTCCACTTCACTGTTACGTTCCCTGTCTCATC[T/C]TTCTAGGTAATTTGAGTTTCCAACC TGTGG
WI-2033	183	T	C	GGTGCTAGA ACTAATCCCTC A	CAGTGGTTCCA CGTTCTCC	ATGTGTATGAGCTCCACATTCGCAGATTCAACCAACTATGGATAGAAAAATATAGTATCCCAGATGG GCAGCCCCAAGGATCAGAGGGCTAAATTTTAAATTTTCAAGGTTATACAGGACCATGTTGGAAATTT AGCATTCTGGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA[T/C]GGAGAACGTGGAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTCTGGTGAAGGACAAGAGTTGAAGCAAAAGGACAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACAGGCTCCTCCACCATTCTCCATCTCTACTCTGA[T/C] AGGCAGACTTATATGGAATAAGGGA
WI-2034	150	T	C	CCACAGTGCA CCAAGGAC CC	GGGTAAGAT AGAGTGCAGGT CC	CCACGACTATGCTTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCCAAGA CCTCCTCTGCGGTTTCAGTGAAGAGACGATGAACCTCTCATCTTCTACAGCAGCTGGACTTCACCA CAGTGCACCAAGGAGT[C/G]GGACCTGCACCTATCTTTACCCCTCCGACACCATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C T	TGTCCTTTAA GTGTGTAAGT ATTAATTAG CA	ATTTCTCTTG AAAGAAACAT CA	TCAGGTGACAAGAAAAAGTCACATTTCTTCAATCACTCACCATTTGCTGTTATTGTCTCTTGCAGTGT ATCCAAAGGATGTCACATTTTGGAACTCTGTAGATCAGAAAAACTGTGCTTTAAAGTGTGAAGTATTA ATTAGATTTCTATTTTGATACTGATGTTTCTTCAAGAGGAAATTTGTGTAAGAGGATCCCAT TGCAATTCATTGGC
WI-4782	113	C T	GATCAGAAG ATAACTAGAA AATGC	GAACTCTCTG GTTATTTTCT GTTG	TCATTGACTTTTAGAGTTCTTCAGTCTTATGTCCTTATTTAGGAAAACTAGGCTAGGAGAA CACAAATTCAGTTCTCTCCAGATGCAGAGATACTAGAAAAATGCCTGAAACAGAAAAATAACCA GAAGAGTTCAATTATGGTTTTTCCAGAACGATTAC
WI-4788	65	A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAAATTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAAATTCAGTGCATAGAAATCATCTTGTCTAAGTTCCAG JTGAAGAAAAATATGCCAAAAATTTAAATTTATCCAACTTTAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
WI-5300	38	T C	TCCAGAGAC CACTTCATTC	CTACTCTTCT ATTTCAATATC CAAAA	CTTACTTCCAAAGTGTTCAGAGAGCCACTTCAATCTCTTTTGGATTATGAATAGAAAGAGT AGGTGTTATTATCTCTTTTACCAAGGTGAAATTTGAGGCTCAGAGACAGGATGATGAGCCCCA AGGTCAGTGCAGAGGCCA
WI-4818b	121	G T	TGATAATGG GCCCTGTT	CCCTCCTTTA TATGTATGCCA GA	TATAATGTTTGTTCATAGTGGCATAGACTAGGTTATGTCCACACATGAATAAACAAATCTTATATA ATAATTTATCAAGAGGAAATATACATATGGGGTGATAATGGGCCCTGTTGCTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43	A G C	TTGCCATAGAC TAGGTTATGTC	CATATGTATAT TTTCTCTCTG ATAAAAT	TATAATGTTTGTTCATAGTGGCATAGACTAGGTTATGTCCAGTGTATGTCCAGTGTATGTCCAGTGT ATAATAATTTATTTCAAGAGGAAATATACATATGGGGTGATAATGGGCCCTGTTGCTCTGGCATA CATATAAAGGAAGGCTAA
WI-5317	139	T C	TTCCATTTCTG GTAGCAGGT	GATGCAAAGA AGAAATGAGTC C	TTTTTCCATTTGTTTGATCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGTTAAT AATATAATAATATGATGTTATATTTACAATTTCAACTCAACAGGAAATTCATTTCTGGTAGCAGGT ATATCTGGACTCATTTCTTGTGATCTATTTCTAGGTTATTTGCAGCCCCGAGATCTACCCAGG
WI-4888	56	G A	GCAAGATATA AAGATTAAAGA AAAGATAACA	CAATTCACCTA CCTCATTTATT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAAATGCTTGATAACTGGAGTAGIGCCTT
WI-5328	44	A G	---	---	AACATTTTTTAACCATGCTACATTTACAAACACTGAAAGACAG[G/A]AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAAGAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATCTGGAAGGAG
WI-4897	93	A G	---	---	GCCTTTTGAGTTTAACTCTTTTGAAGTGTCTTTTTTTCCCCACTAGGTACTCTCGGCCCAAT CCCCAAAGAAAAAAGCGCTTGG[G/G]GATAAACACATCTTC
WI-5345	29	G A	---	---	CCCTGCTATAGGTCAGTTTAAAAATCCT[G/A]CCTGCTATGGTTGCTTGTGAAGCCACATCCACT GAGGTATATCTGTCTGCATTTTCTATATCACTCAGCTTCAGATCCACTCCATCAACTTGCAG



TIGR- A004W22	232	C A	---			GGATAATCAGTACAATAATGGGACCTTTAAACTGCTGTGATGCAGGAGTGGAGGGCTGGGCGAGTG CCGAGGAGGGGAGGAGCAGTGGGACAAGGGATGCTCAGTGGTGGAGCCACAGCCCTGGGCTCTGGA TGGGCATGGGAATGACCAGGTTCCACATCATGCACAGCAGGGCCTGTAGCTTGAGTCCAGACAG GCCTGCCACATTTGGTCTGCCCGCCCTAC/AJCTGGAGATGCTCTAAAA
TIGR- A005D24 b	138	C T	---			CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAATTCCTTTGAGATAATTGATTCATATTC TGCGCTTTC AACCTCATTACCTCTGTGATTC AACATCTTTATAGAGAAATAGAAACCCAAATTT CTC/TJTTTCCACATTTAGTTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACTTTAATAATTAGGAAACAAT
TIGR- A005D24 a	123	A G	---			CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAATTCCTTTGAGATAATTGATTCATATTC TGTGGCTTTC AACCTCATTACCTCTGTGATTC AACATCTTTATAGAGAAATAGAAACCCAA TTCTCTTTCACCATTTAGTTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATT TTATGTTAAATTCATAAACTCCTTCACTTTAATAATTAGGAAACAAT
U03735	74	C G	---			TGAGTGTGACGAGTTGCAGCAGGGCCAGTGGAGGGTCTGGCCAGTGCACCTTCGGGGCC GCATCC/CGTTAGTTTCCACTGCCTCTGTGACGTGAGGCCATCTTCTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGTTCTGTTCTGTTGGATGACTTGAGATTATCTTTGTTCTCTGTTTGA GTTGTTCAAATGTTCTTTTAA
U39840b	42	T C	---			GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAT/CJACACAGCAAAACCAACCACA CAACCAAAACCGTCAACAGCATATAAAATCCAAACATATTTTATTTCACTTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATGTTTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTC
U39840	56	A C	---			GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAATCAACAGCAAAACCAAC/AJACCCACA CAACCAAAACCGTCAACAGCATATAAAATCCAAACATATTTTATTTCACTTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATGTTTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTC
WI-8997	41	G A	CCCC			GTGGCCATCGATCTGGACCGTCCCTGCCACTTGTCTCCCG/GATGAGCACTGCGTACAAACATCCA AAAGTTCAACACACACAGAACTGTGTCTCATGGT
WI-7008	180	A G	---			TATACCACTTCCATTTGATGATGGAATGCTGCTGTTTCATGACCAACCTTTATGGCTAGATGGGTGAGAA AGCACCCAGTTTCATGATAGGAGTTTCAGGTATATGGTACTTGATGACCCAGAGTCAACATTTCAG TTTCCACCAAGCCCCAGTAACAGGCCAAGAGCTGTCTCTCAAAAG/AJGAGAGTAGTATCTGCAGA AGATGGCAGGGCTTGTCTCCGAAAGCCTAGAGCCGCACTGTGATTCACCT
WI-9005	26	C T	GGGAATCT			GGTCCCACGAATTTGCTGGGGAATCTC/TJGTTTTTCTTCTTAAGACTTTTGGGACATGGTTTGACTCC CGAACATCACCCAGCGTCTCTGTTTTCTGGTGG

WI-7593	46 G A ...	---	TTTTTGTCTGGACACCCACTGCTCCAGGATGAAAGGAGAG/GAATGAGATCAGTTTTGGA CACTTCCTCTTGAAATATAAGAAATCAACAAGTTACAGTCATGTTGGGACTTCTTCTCTCCAA AGTGATCTTGGGGAAAGGCTCCAGTGTATCTGGACAGTCTCTTCAATTTTCAGGTGGGACTCTT GATCCAGAGAG/GAGCAAAAGCTCCTCAGTGAGCTGGTGATATCCAAAGACAGAACCCCAAGTCTCC TGACTCTGGCTTCTATGCCCTCTATCCTATCATAGATAACATCTCCACAGCCTCACTTCAATCCAC CTATCTCTGAAATATTCCTGAGAGAAACAGAGATTTAGATAAGA GCAGAGAAGAGAACCATGCCAGGGGAGAGGCCACCCAGCCATC/GJTGACCCAGCGAGAGCCAA CTATCCCAATATACCTGGGTGAATATACCAAATCTGCATCTCCAGAGGAAATAGAAATATAA GATGAATTGTGCAACTCTTAAAAA
WI-6962	78 A G ...	---	AGCAGCCATCACATGATCTGTTTTTACCACCTTCACTGAAAGACACCATTTAT/CTACCCCAAGGG CAGAAAGTAGAACCTTACTATTCAATAATGTTTGACACAATTTGGAATTGTC AAGGGCATTGAGACTATAAAGCAGTAGACAATCCACATACCATCTGTAGAGTTGGAACCTGCATT CTTTAAAGTTTTATATGCATATATTTAGGGCTGTAGACTTACTTCTTATTTCTTTCCATTGCT TATCTTGAGCACAAATGATAATCAATTATACATTTATACATCACCTTTTGTGACTTTTCCAAAGCCC TTTTACAGCTCTGGCAATTTCTCGCTAGGCCCTGTGAGGTAACCTGGAT
WI-7079	293 T G ...	---	TGGATGCCGAGGTAAAGTTCTTTTGTCTATAAAGAA/GAAGGAACCTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAGGATGTGCCACTGGCAATGTAACGTG GGAGTTGCCCTTCTAAGGAAGGAGATCTTATCTTCTGGTTGGCTTGACCACTACGTTGGGA GAAGAGAGAGAGTCCAGGAGACCTGAGGGCAGCCGTTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGCCACCAAGAGGGCTTGGTTCTGAGGAAGCAGATGTTTCATGCT GTAGGCCCTTGACCCAGGTGGGGCCACAGCACCCAGCAGCATCTTG/C/JT GGAGTTGCCCTTCTAAGGAAGGAGATCTTATCTTCTGGTTGGCTTGACCACTACGTTGGGA GAAGAGAGAGAGTCCAGGAGACCTGAGGGCAGCCGTTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGCCACCAAGAGGGCTTGGTTCTGAGGAAGCAGATGTTTCAT GCTGTAGGCCCTTGACCCAGGTGGGGCCACAGCACCCAGCAGCATCTTTGCT CATAAATGAGAGCCCTGAGCCCTCAAGAACTCA/CJTGCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTTCATGCAAGGGCAAAAGGCAAGTGCATGCAAGCTGTTAA
WI-7104	157 C A ...	---	CTGTAGGGTGTAGCTAGCATTACCCCAACCTCATTTTAGTTGCCTAAGCATTGCCTGGC/C/JTTC CTGTAGTCTCTCTCTGTAAAGCCAAAGAAATGAACATTCCA CCCTGTTCCCATGCTGACCTGTGTTTCTCTCCCAAGTCACTTTCTGTTCCAGAGAGGTGGGCTGGAT GTCTCCATCTCTGTCTCAACTTTAT/CJGTGCACTGAGCTGCAACTTCT
WI-7104b	249 C T ...	---	
WI-7104	157 C A ...	---	
WI-8974	34 C T	---	
WI-9161	61 C T	---	
WI-9014c	93 T C	---	

WI-9014b	44	C T	---	---	COCTGTTCCCATGCTGACCTGTGTTTCTCTCCAGTCATCTTTC/TGTTCCAGAGAGGTGGGGCTG GATGCTCCATCTCTGCTCAACTTTATGTGCACTGAGCTGCACTTCT
WI-7023b	206	C A	---	---	TCTGAGAGAAATGACTTGTGGAGACACCTGCAGATCCTCATGGTTGTGACAGACCTGCGTGCT CAGTGCCCTTTAAGTGCATCCGCTGTGCTGACTTTGAGTGGATCAACATCTGCTCAGGGTCCCC TCTTTTGGCCCCAGTATTCATGGCAGGGTTGTTGGACACCTACTAGCTTCCCTTCCCATCAACAC A/C/AJACACACATCTTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56	A C	---	---	TCTGAGAGAAATGACTTGTGGAGACACCTGCAGATCCTCATGGTTGTGACAG/A/CJCCCTGGGT GCTCAGTGCCCTTTAAGTGCATCCGCTGTGCTGACTTTGAGTGGATCAACATCTGCTCAGGGTCC CCCTCTTTTGGCCCCAGTATTCATGGCAGGGTTGTTGGACACCTACTAGCTTCCCTTCCCATTCAA CACACACACATCTTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54	C T	---	---	CTGAATCCCCCTCTCTGCCCTGGCTGGATCCGGGACCCCTTGGCCCTCCCTCTGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTGCCGACCTCTCTGGGCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAAGTTGTGTGAAGCAGAGAGAAAGCTGGAGGAGCCGTGGGCCAAT GGGAGAGCTCTTGTATTATTAATATTGTGGCGCTGTGTGTGTGTTA
WI-9171	62	G A	---	---	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAGAAAGTAGAGATAATAATCA[G/A] TTCTTTACAACCGATGGTAATTAAAGCTTGATTCAACAGACTTCATGC
WI-9174	47	T C T	---	---	GTGTGAGACCATCATGTGGCCAGCTAGGACCCCATCTCTCTATTATTCAGTCCTGTCTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAATTGAG
WI-7753	52	A G	---	---	AAGCCAGATGCACATCCCTGGAGGAGATCCATGTTCCGAGAGAAACAGATTA/GJATCCCTGTATT TCAAGACCTCTGTGCACTTATTTATGAACCTGCCCTGCTCCACAGACACAGCAATTCCTCAGGCTA AGCTGCCGGTCTTAAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76	G A	---	---	AAAGAACTACAGAGGAGGATGTCCAAACAAAAATGGCATCACCTGTCAAAAAATGGAGTTCCACT TCTCCCCGCA[G/A]ACCTAGGTGAGACTTCCCTTTTCATCTT
WI-9193	94	G A	---	---	TTGGACAAACCTAGAAATTTCTCCCTTATGTATCTCTATOGATTGTAGCAATTGACAGAGAAATAA CTCAGAAATATTGTCTGCCTTAAAGCA[G/A]TACCCCTTACCACACACACCCCTGCTCTC
WI-9015	48	C T	---	---	TTTGGATTGATATCGTGAATCTCAGCCGAGAAATTTGGGCTGGATTG[C/T]GCTTTGGTTATACAT CTTTCCCTAAAGAGAGATAAACACAAATCCATTCAGGTAGCTCGGCACCACTAAGAA
WI-7254	37	A G	---	---	GGAGCCAGGAGACAGAGGGTCTGAGAGAGGAGCCAC[G]GTCCCTAATGACACCCACTCCTAGCC CTGAGGCTGTGCCCTCAGACTGGGGAAGAGTCCAAAGGAAGGGAGGAGCAGCCACTCCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG





WI-9281	68	G A	---		---	ACTGGTGGGAGACTGTGAGGATCCAGGATTCAGTATTCCTGGCCAGAGGGCCTTCTGGCTACTGG [G]ATGTTAGTTGCAGTCTGTGCTCCCTCTCTATGACTGTGCCC
			GCTAACACTTT TTAAACCCTG CTC		CATTTATTTG AAAGCTATTCA GACA	TTCTGAAATATAACAGCCATTGAGCTATTTAAACCTTGTAATTTTAAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTGCATCTCGTGACATAAAACATTAATGCTAACACTTTTAA ACCGTCTC[A/G]GTCTGAATAGCTTCAAAATAAATGGAATGGT
WI-7848	142	A G		GTATATTACA ATGATCACCG ACTGA	CCCCACAGAAC TATTGTAAAC AA	TCACGTTTGGTCTCTCAGATTCTGAGGAAATGCTTTGATTGATATTACAATGATCACCGACT GA[G/A]AATATTGTTTACAATAGTTCTGTGGGCTGTTTTTGT
WI-9304	70	G A				TTACAGAACTTCCCTGTGCCTGTGCCCATGCTAGGGCGGAGGGTCTTTCCCTCTCTTTCC TACCTACCCCTTTTCTTGGCCAGGGCTGATCTACCTTTCTTGTCCCTGGGCTGGCTGCAC AGAGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGACAA AGTCTAAGGGACCATGGCTGCCCTTGGGAGGAACCATAGCTCCCT
WI-7933b	314	C A	---		---	TTACAGAACTTCCCTGTGCCTGTGCCCATGCTAGGGCGGAGGGTCTTTCCCTCTCTTTCC TACCTACCCCTTTTCTTGGCCAGGG[G/C]CTCGTATCTACCTTTCTTGTCCCTGGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGCA CAAAGTCTAAGGGACCATGGCTGCCCTTGGGAGGAACCATAGCT
WI-7933	96	G C	---		---	CCAGATGTCCCATCACGTTTTCTGAGGCTTTGTACTTTAGTAAATGCTTCCACTAACTGAAA CCATGGTGAGAAAGTTGACTTTGTTAAATATTTGAAATGTAATGAAAGAGTACTGTATATTA AAAGTTGGTTGAACCAACTTCTAGCTGCTGTGAAGAATATATTG[T/A]CAGAAACACAAAGGCTT GAT
WI-7374	182	T A	---		---	
			CCAACAACAT CCTCTGCCA		AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCCTGCTACCTTGACCCCTTCCCTTCTCTCTCTCATCATCATCTCCCAACAACAT CCTCTGCCA[C/T]ACACAACAACAGTAAGTTTCATTTGGGCAAA
WI-9343	78	C T				CTATATGTGAGAGCGGTATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAACAATTTGTTA[T/A]GTGTTTAGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-7386b	104	T A	---		---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAACCTGAAGAGTTCACTTTGTATTAT GCTCTT[A/G]TGATTACAGACTGATGCCAGACAACCTTGGGAAGA
WI-9357	75	A G	---		---	TGAAGGGGTGTGGCATCTGTGTTTCTGATGCTTACTACAATATGGAACCACTACTTTAGAAAACTGT CTTTAACTTGGT[C/J]ATTCCTCTAATTGTGTTCCCTAGGAAATGACTGICCCAAG
			CTTTAGAAAA TCTGCTTTAAC TTGG		CCTAGGGAACA CAATTAGAGGA A	TGCTCCCTGTCCCATCTGCAGTGGACCCAGGCCACCCCTTTGAGGAGGTGGGTGAACGTCTCCTT GGCAGGGATTTGTGACACTGCATTGCTGGGTGTTCC[T/C]GGGCTCTTCTGGACCTTGCACCGTG GATACCAGGCCATGTGCCATGGTATTGGGTCTCTGGGAGGGTGGGTGAAATAAAGGCATCTGTCT
WI-9360	79	T C				
			TGCTGGGCTGT		GGTCCAGAAGA GCGG	
WI-7423	107	T C				



WI-9448	184	G A	---			TGGGGCTGCTTTAGACTTCATTTCTAGAGCAGACACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCTTGCCCATGGTGTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAATGGGCTTGTTCCAAAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCCTGCTTGATTTTATCCAAAGGCTGTTCTTAACGTGCCGIGAGCAG
WI-9470	204	G A	---			ATGTCAGAAGAGACACAGACAAGGAGTTTTCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAGTACAGCTCTCCAGGTTGATAAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGGAATATGATCTCCCTAAAGCCCAAGATTCCTACTAGAGCCGCTGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACCAAGGCTCACCTTCCCAG
WI-1245b	201	G T	---			GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGTGCCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAATTTCAATTTATCATCTGACAGCCCTTCTTTAAGTACATCCTTGCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C	---			GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGG[T/C]GCCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGT GGTTTAAATTTCAATTTATCATCTGACAGCCCTTCTTTAAGTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A	---			TTCAAGTAAAGGACAGGTCTAGAACAGCGTTCCTCAACCTGGCACCATGACAGTTTGGACCAAA TAATCTTTGTTTTCAGGGGACTGTCTTACACATTTGTGGGATTTTACAGCCCTCCGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACCCCTCCCCAACAAATCATGACAATGAAAATGCTTTTAGACATT GCCAAATATACCTTGTGGGACAAAATGGCCCTGATTGAGAACCACTGGTT
WI-5385	110	G A	---			AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAATGGTGGGATTTGAAGAGG GAAGTCGATAATTTAACATATGGTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCTTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCTGAC CCCTGCTACGGGAAACATTGAATGCA
WI-5403	199	T G	---			ACCAACCGTTGGCAAGGCTCCCAAGACTCACCAACCTTGGTGTACCCTATGCCGGGTG GGATTGAAGAAATAACCAATAAATGCTACAAATTTCCAGTAGTTACAGGCACCGCCTAT TGGAAGAAATCAATAATGTAACCTACAATGATTTGCTCTGCTGGCTGGTCCAGGCATAGAGTT/G JGGCTACAACCCATTTTATCATTTGAACCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G A	---			TGGTATTTTCTTTCTTAAATGTTATGATTAATTAGTGCTTTGTAGAAATTTGAAAAATGTAAA TCAGAGAACAGAGAAAAATAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]AGGGAATGAGAAAAAGCACCAACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCCAAGGAAGTTAAGT

WI-5801a	48 A G ---	---	TGGTATTTTCCCTTAAATGTTATGATTAATTAGTGTCTTTGTA/GJGAATTTGAAAAAATGT AAATCAGAGAACAGAAAAAATAAGTATAGTTGAAACCTCTAAACAATTTTAGATTTTAAAGGCC TAGGGAAAGAAAGAGAGCCTGGGAAGAGGGAATGAGAAAAGCACAACCAAGAAAAAAGTGTGT GGCTTAAGGGAGCCAAAGAAAGTTAAGT
WI-5696	61 C A ---	---	TTCTATTTAAATCCTGTGCCCATTTGCAAGACTGCATTAGTCTGCATGAGCCTTAGTTTC/AJTA AAGCCCCCTCACACCGAGGGACAATGTTCAAGAACTAAATGACTGAGGTGAGCAATCTCTGTATTA TACAACTGGGACCAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGTGAGTTTATTTAACTT
WI-7461	153 C T ---	---	TATTACTAGGTTTCATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATCTAACGCTCCTCACTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGGACTGTGTCTC/TGTCCCTGTTGGGTCCCGAACCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCAITGTCTGCA
WI-9716	221 G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAATCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCTTTTGGTATACCTTCTCTTCTGAAGACCAACCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTTCAGATGTGTACTTCTACATTCGAAACACTAGATGAGTAGGCTCTCTTCATCT CAATTGAAAATCTAGAA/GJA/AAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49 C T ---	---	TTTTCGTTAAGTCTTGGAAGCCACACAGAAAGTGATCTACTCTCTTAC/C/TAAGTGTACTTTGCA TATATTTATGGGATGATTTCTATCCCTACTTAAGATTTCTCTCTCAGGTTAAATATCCATTCCT TTGTTCAAGGAGTTCTTATTTGGCTTCTTTCTAAACCTTAACCATTCGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---	---	GAAAACCTCGTTGGCTCAAAGGAACTGTAG/A/CJAAATCTTTTTTTTATTTTGTTTTAACTC AAAGAGTGGAGTTTGCATTGACCTTGTGATGGCAGCTGCTCTTTGTTTGGTAAATCCCTTAGT GGGCACCTTGCAAAAGCAATTTAGAGCAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAG TAGCAATGGAAGAAAGTTAATGGA
WI-10312	41 A G ---	---	AAGGCCAGTGGGAAAAAGCAGACAAAAACACTCCAAGAATAC/A/GJAGATAAAACATCATCA GTAGAGATGGGATGACCTAGGAGGTCTGCTGATGAGGGCATGTAGACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGGTGAGTCTGCCAGTCCCATAGTAGGTGTTCCATAAATAAAC AGTGACTAACTGAGGTAGAGTCACAGAAAGAAATTTCA
WI-11152	179 C T ---	---	GATTCCTTTGGACATGCAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAAACGAGCCCTA ATTCATAGAAACAGACTCTACAAGGACCAGTTAAAGGTCTGCACCCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGGACAAAGTGGGACAAAAGGCTTGTCA/C/TTGTCTCAGAAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167 A G ---	---	TGGTGGAGCTGTAAAGCTGAAAGAATAGTCTCTGCTGCTGCTTTCGGTGGAAATGGATGAGTCCT TTTACAAAATTTTCCCTCTGCCATGGGTGTTATGTTTAGAATCATGGAGTTGGAAGACTTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTGTA/GTGAACCTTGAGCAAGTGCTCTTAATGTCCTCA GCCCAATGCCCTTCCCTGTAA
WI-4701	198 G A ---	---	GGGTTCAATTTAACAGCCTCCCACTGGGTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGGCCCACTATTGACTTGATAACACCTACAAACAACACATTAAACCTCCTCCCACTCTA CCCGCAAGTCTACCTTTTGGTCTTTTATTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCATTTTCAGAAAAGCAGTATA
WI-4823	164 C A ---	---	TTTATCTTCCAAACCATGTGTGTTTTCTTCACATACITTTACGTAAATTTAAATCATGTCATTTAATTA TGCACCTACTTGTGGCTACAGACATTTGCTTCCAAATTTGTAATCCCTAACACAGCAAGCATAACT GATGTGCCATCTTTGTATTCTTAAAC[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCTCTCTGT CTTCTCTGTTTCACCTCCTGTATTTCCTTATTCAGCATTCATGATTA
WI-4860	72 A G ---	---	AAAAAACAACCTTCATTGACATCTAAGAAAGATAAAGAAAACAACGATCCACTGTGTGTTGCTTT GATTTA/GGGAGATAAAACCTGATCTTAAGAAAATTAACCAAAGCAGTACACTAAAATAGCCT TTGTGTGGTTTTTCAGGAAGAAAGCCAAATCCAACTAAGTTGCTAAGAAAATAATGTTTCATATCA CTCTAACTTCCACATAGAGCAATTAATAGCA
WI-9705	111 C A ---	---	TGAAAGGACCAGTTTCAATGCTTACCAAGGTAAAGTAAATCGGAGGGGCGAGGAGTGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCCGCTGCC[C/A]AAAATTTGTTAACACTGATGC TGCTACAAACGCACATAGAAATCGGTGGTAGATTGCGGTTCTCTAGTAGCTAATGTTTAGATA TGATTGTTGAATTAATGTTGCTGTGTTCTTGGTG
TIGR- A004Z48	177 A G ---	---	CAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTTCATGTAAGGTGGGCGAGGGTGGACTG AAGATCTGTTGGCAGGCTCACAGAGACGGGGGTGAGGGGAGAGATCGTGGTTTCATGAGATCCCAT CTTGGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGA/GTCCCTCCAATTCAGGGGCTCCC GTGGGATGTTGGAGCCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
U17579	34 T G ---	---	GGGATTCATGTGTCTGTCTCATCCAATAAGCACT/GJCATGACCTCAGCCCCATCTCTTCTCCC TATGTTCCAGAGACAGATAGACCTGGCCCCCTTCTCTAGGGGATCACATAATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGGAGAGGGATCCTTCTAGTTGA
WI-7747b	88 T G ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGCTTTCGTTAACTGTGTATGACATA TATATATTTTAAATTTGAT/GJAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTTCTGTTGTTGTTGGGTATCCTGCCAGTGTGTTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCATTGTAAATAAGTATATAATTTTTATGTTTTGTTCTGA

WI-7747a	44	T C ---	---	GTGAGAGGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGGT/CJTTCGTTAACTGTTGATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAGTT ATTTCTTTGTTGTTTGGTATCTGCCCAGCTGTTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCATTGTATAAAGTATATAATTTTATGTTTGTTCCTGA
WI-7189	197	T C ---	---	TCCAGAAATTTCTCTTCAGCTCATTTTGCTCTCACAATTAAGGGAGTAGGTTAAGTGAAAGGT CACATACCATTAATTTCCCTTCAACAAATAATATTTTACAGAAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTATTTTATATTAAGCCTACAACATTTTTC/CJAG TTTGCAATAGAACTAATACTGGTGAAATTTACCTAAACCTTGGTTAAT
WI-7850	57	G A ---	---	AGCCGAGCTGGACTCATGGATGTGCACCTTTGCTCCCTGCTCTTCTGCCTCTGG/CJCTCATGTA TCTGCGCAGCTCTGTACCTCTGTGGTGGCATCTCTACCTCTGACACAGACTGCCTGCCTTGAAGCT GAGAAAGCACAGGGCAAGGAGCCAAAGGACACAGAGCCTCAGCCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAATCAGGGGGCTGTCTACTAGAGCC
WI-7907	69	G C ---	---	CTCTCTCTTCATCCCATCACCCCTAAATAGGTCAGGTGAGGGAGGCTGGGAAGAGGTGGGAGGAGG G/G/CJAGAAAGTGAAGGAAGATAGGAAGGATATTACCTCTTCTGTTATTTTAAAGAACATTGTTT GGTGGCAGCAATCTCCCTGTCCTATCATCTGTAGAGGCTTAATTTTATATCTATAAATATATTAAVA AGCAAGTCAAACTTGGATGATCAAGGTAAATATTGTCAAAAGTTAAAT
WI-7919	242	T C ---	---	GAAGGAGCTGGATCACTTCCCGCAGTCTTGGCAGGCTTTGCTGTGGAACACAGAGCTCCTCCT CAGGGGCTGGCAGCTACCTTCTATTCTGTATGATGATGATTTGTTAAACACAGTCAAAATAAGAGAT GTGCCAGATTTAGATTTCTTACCCTAATCTGTTTAAATTTGTAACCTTATCCCATTTGAAAGTGCA AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAAT/CJACAACCTT
WI-7928	101	T G ---	---	CTCCCTTCTATGCTCTCAGCAGCAGTGGGGCACACTTGTTCATCTTCTGACCGTTTGTGGGCTA TTCCCTGCGAGTGACAGACATCGTCAAAATTCAT/GJACAAGAGGAAATTTTCAATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACTTTAAACTGAAATCAACTCTTTATATAGGATTTTCTTTT CTATCTCCATCTCCTCATTAAAAAATACGTACATTTGAGGTAATGGTA
WI-7936	131	T A ---	---	TTTTGAGTCAAGACTTAAAGGGCCCAATGAATATTATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATTTCTTTGGAGTTAAATGCACATATAGACACATACCCCAACACTTACACCAAACT/A ACTGAATGAAGAAGTATTTGGTAACAGGCCATTTTGGTGGGAATCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99	T C ---	---	TACACGTTCCAGCCCGTTGCCCACTCATCTGCGGCTTTGCTTTTGGTGGGGGCGAGATTGGTTGG AATGCTTTCCATCTCCAGGAGACTTTTCACTG/CJAGCCCAAGTACAGCCTGGACCAACCCCTGGTGTG TGAGCTAGTAAGATTACCTGAGCTGCAGCTGAGCCTGAGCCCAATGGGACAGTTACACTTGACAGA CAAAGATGGTGGAGATTGGCATGCCATTGAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---			TTTCTAGGCTGTACAGTCTGATGCATGATTTTTTATAAAATTTTCATACCTTGTGAATTTGGATCTT TTTACTTTGAGCATATATTTAGAATATGTGT/GJTGTTAAAGGATCTCCACAATGTCTGCAGTGTG AAGCAGGTTTCATTGTGAATAGTTAACAGTCAGGAAGGCTAAACTGGTCAGTATTAAATGTGTAGC CCTACCAAAATAGCCAGTAGTATCTGAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---			GGCCAGGAGATTAGCAACAAGGATTCTGTTACTTACTTGGCCCTTTTATCTTCCCTCTTGCCC CAGTCCCTTCTCCAGCTTCATGTGAAGCTCTGCACAGACAGACAGTCTGCTCTTGGCAGTGCT [G/J]CTACTCCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTGGCAATGTCATCAG
WI-140	252 C T ---			ATTTGAAGATTGGAGGCTTGCAGAGGAAATAGATTTCAATTTGGATCCCCCAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAGTGAAATGCAAGTTGTACCAGTAAAGTTTATA TCTTCCATTCAGCCAGCTCATTTGCCAGAAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAAATTTAGTTAAAAATGTGTCATTTGTCGTGATTGGCATTCCJ[C/
WI-198	218 C T ---			GAGGCTTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTTCCCGGATCAAGTCTGGCACC CATGATGGAACCTCTGCCATGGTTTTAGTACCCCTGGACCAAGTAGTATCCATCCTGACTTTAAAA TTCTAAACAGCCCTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCTTATCTTATCTTCAGCTA CCTGCTCCCTTTCTC/JTGTTTAAACAAAGCATAGAAATATTCTGAACAAC
WI-205c	146 T C ---			TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAATAAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTG/JCJCCAAAGGCTTGATGGGAAAAATCTCAACATTTGTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATAGCCCTTTATTTTGTAGTCC
WI-205b	146 T C ---			TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAATAAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTG/JCJCCAAAGGCTTGATGGGAAAAATCTCAACATTTGTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATAGCCCTTTATTTTGTAGTCC
WI-234	165 G C ---			GAAGACTGAGTTTCCAGGAGGTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCACCCCAAGTNCITTTCCAGAGGCTCAGACTACCTCCTCATCTCCCT CTCCCCACAACACACAAATACAGAGATT[G/JAATTCAGGAGCCAGTTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTCTTAGTTTCTCAATGGGAAATGG
WI-276b	25 A G ---			AGCTTTTGAATCCAAAAACACAT/GJCTTGACTCTCTTATCTCCTCTTGTGTAACTATATCC CTGAGGAGAAATACAGAACACCCCTGTGGCTGCTGAACGGAGGAGGATGGGGGGGGGAGACAT CGGTCAATGTATCAAAAGCATCTCTCTGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTATCCTCTTGTCTATCCCTGATGACTGGGCAA



WI-276	25 A G ---	---	AGCTTTGAAATCCAAACCACATAGJCTTGACTCTCTTATCCTCCTCTTGTGTAACATCTATCC CTGAGGCAGAAAATACAGAACACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAAGCATCTCTCGCCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTATCCTCTGCTATCCCTGATGACTGGGCAAA
WI-427	59 G A ---	---	TTTCCCAATCCACAGGTAAACTAATAATGGATGTATAGAAITTAGAACTACTTCQIGJGTTTT TTCCCTGGGAAATATTCACAAAACATTTGTGGTCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCATTTATTAGAGCCAGGGTCTGCTCTGTCACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	CTCTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCCGAGAAAGGCGCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---	---	CTCTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCCGAGAAAGGCGCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---	---	CTCTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCCGAGAAAGGCGCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---	---	GTGTAATTTGGTGGCTTTCGCACTTTCCACAGTAACCTTTAGAAATNNAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATGJAGJTAATGACCCCTCCATGACTCTGGTACCTCATCATTAACCAATGTGAGAATTATTAAC TTGAICTAATATCTTCACAACATAATACCTGAGAGAAATAAGICTATTTAAT
WI-597b	141 A G ---	---	GTGTAATTTGGTGGCTTTCGCACTTTCCACAGTAACCTTTAGAAATNNAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATGJAGJTAATGACCCCTCCATGACTCTGGTACCTCATCATTAACCAATGTGAGAATTATTAAC TTGATCTAATATCTTCACAACATAATACCTGAGAGAAATAAGICTATTTAAT
WI-597	136 A G ---	---	GTGTAATTTGGTGGCTTTCGCACTTTCCACAGTAACCTTTAGAAATNNAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATAGCATGATAATGACCCCTCCATGACTCTGGTACCTCATCATTAACCAATGTGAGAATTATTAAC TTGATCTAATATCTTCACAACATAATACCTGAGAGAAATAAGICTATTTAAT

WI-611	66 G C ---	---		TTCAAAATTAACACCATTTGGGTATATTAAATTTNGCTCTATCCATAGTTCTAACCCCTCTCTCTG/CJACAGTGAGACACCTGCTCTCTATTGTCTTGACGTATTACGTATTCGATCAGTACCCCATCTGGAACCAAGGTTTCATTTCTGCTGACCCCTCCCTCTCACCCCTACTTTGGGCTCTGACTTCTCTTCTCTGGGCTGAACCTCTCTGTGTGGCTGTCGGCTTCTCTGCTTGGGCTTCCAAATAC
WI-681b	156 A G ---	---		TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATTCATAAGTTCATACAGGGGAAGACTTTGNCCTGGTATGTGCATAAGCAA TCCATAATTGTTATAGCTATTAGJTATACATATGGACCAATTTGGACACAGATTATATATGTACAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCAATGGTTT
WI-681	156 A G ---	---		TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATTCATAAGTTCATACAGGGGAAGACTTTGNCCTGGTATGTGCATAAGCAA TCCATAATTGTTATAGCTATTAGJTATACATATGGACCAATTTGGACACAGATTATATATGTACAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCAATGGTTT
WI-867b	119 G A ---	---		AATCTTAACAGCCTTTTGATGCCAAAGCCACTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCTCCAAGGCTCCCGATATCTGGCACATCTTCCCTTTTCATCTCCG/AJTTGTGTGTTGGC CAATAAATATCTCCCGAGGACGTCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGCG AGTGCTATGGTTTGAATGTGTCCCCCAAAAGCACACATTAGAAACTTA
WI-867	113 A G ---	---		AATCTTAACAGCCTTTTGATGCCAAAGCCACTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCTCCAAGGCTCCCGATATCTGGCACATCTTCCCTTTTCATCTCCG/AJTTGTGTGTTGGC CAATAAATATCTCCCGAGGACGTCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGCG AGTGCTATGGTTTGAATGTGTCCCCCAAAAGCACACATTAGAAACTTA
WI-867	119 G A ---	---		AATCTTAACAGCCTTTTGATGCCAAAGCCACTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCTCCAAGGCTCCCGATATCTGGCACATCTTCCCTTTTCATCTCCG/AJTTGTGTGTTGGC CAATAAATATCTCCCGAGGACGTCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGCG AGTGCTATGGTTTGAATGTGTCCCCCAAAAGCACACATTAGAAACTTA
WI-871b	123 C G ---	---		TCATCAGACCTGAGATTGAGCATGAAATCTACCAAGGTACCAAAATGTAAACCTTGTCCTCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCACCCACCTACCTCATG/C/GJAACCTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAAATGACACTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCAATATGNCCTGATTGTACATAA
WI-871	123 C G ---	---		TCATCAGACCTGAGATTGAGCATGAAATCTACCAAGGTACCAAAATGTAAACCTTGTCCTCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCACCCACCTACCTCATG/C/GJAACCTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAAATGACACTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCAATATGNCCTGATTGTACATAA

WI-884	198 T C ---	---	AGGTTCTGGACTTGATGCTGGGAAACAATGGGTNCTGGAGAAATCCTATTTGAGTNTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAAGTTCTCTGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAAGGAATAIT/CJG ATCCCGCATGCAACATTTATTCAGTGAAACATGATGAAAATGAACATAAT
WI-921b	205 G A ---	---	CACCTCCAAAGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTATACTGG CAGTGATGCCCTCTCACGCCCTGGCCCCCAAGAAAGTCTTGCCAGGAAAAGCAGCATCCATCTAC TCTG/AJGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTTCCGAG
WI-921	205 G A ---	---	CACCTCCAAAGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTATACTGG CAGTGATGCCCTCTCACGCCCTGGCCCCCAAGAAAGTCTTGCCAGGAAAAGCAGCATCCATCTAC TCTG/AJGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTTCCGAG
WI-945c	90 G C ---	---	GGCTGGGATGAGAGGTCTACTTTGTGTACTGGAGTTTCACTGGCTTGCTAGAACTAGNAAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCAAGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAAATCTCTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-945b	90 G C ---	---	GGCTGGGATGAGAGGTCTACTTTGTGTACTGGAGTTTCACTGGCTTGCTAGAACTAGNAAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCAAGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAAATCTCTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-960b	167 C T ---	---	TTGCTTCAAAGAAAGTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATGTTTTTGGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 G A ---	---	TTGCTTCAAAGAAAGTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATGTTTTTGGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 T C ---	---	TCCCACTGAGTATGGCTTTCAGTAGTTTTTATTATGATGTGCCTAGGTACATTTGTTTTATTGTTCTG CGAATTGTTGATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCCTTTCTGTGTTG CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCACTA[T/C]GCTGTTTTTACTCTCCTCTG ATTTTTTTCCATTATTTTTATTGCTCTGGCTTCATTTTGTAATNTG

WI-1147b	204 G A ---	---	---	TTGCCATTATTTGAAGATAACCCACACCTTGGTGTCAGGGTTTTCACAGGATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCCAGCCACCGCAACTTCTCCTCCCTGGCTC CTGAGCCAAAACAGGCATTTACCATAAATCACCTTTGTTAGGATGAATTAATCTGGCCAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147 C T ---	---	---	GCATTCAGAGGTTGTTAATGACATTCACGTAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAATACAAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT TAAGTCTGGGG/C/TJCTGGGGTCAGGCTGCCTGGGTACACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124 C G ---	---	---	GCATTCAGAGGTTGTTAATGACATTCACGTAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAATACAAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT GGCTAAGTCTGGGGCTCTGGGGTCAGGCTGCCTGGGTACACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124 T C ---	---	---	AAGTTTACAGAAAAAATACCAGAAAAAGTGACITTCAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTNCACACAGACACTTATCCCTAGACAGCCATTTCTTTTGAATG/T/C/GNCANT AAAAATGATTTGAAATTTGGGAATAAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTTGCCTAG GCC
WI-1305d	202 C T ---	---	---	TTCTCAATTCCTCAATCTGTGTACTTTTATTTCTTTCTTTCCATT/C/TJATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTTCTCTC TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNTATG/C /TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46 C T ---	---	---	TTCTCAATTCCTCAATCTGTGTACTTTTATTTCTTTCTTTCCATT/C/TJATGTTGGTAAATATAAAG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTTCTCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNTATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153 T C ---	---	---	TTCTCAATTCCTCAATCTGTGTACTTTTATTTCTTTCTTTCCATT/C/TJATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTTCTCTC TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNTATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202 C T ---	---	---	TTCTCAATTCCTCAATCTGTGTACTTTTATTTCTTTCTTTCCATT/C/TJATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTTCTCTC TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNTATG/C /TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248 A G ---			TTTCTGCATTGGAATAGTTGACCTTCTATGAGNNNGCAATAATAATGGACAATCTTGNGNNNNTNG GGCTGGGTGACTGTGCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTCTCTA/G/G/C
WI-1306	240 A G ---			TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAATCTTGNGNNNNTNG GGCTGGGTGACTGTGCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTA/G/JTCTCTAGC
WI-1307b	118 T C ---			GACAAGGCTGGTACTAGTTTCCAAATCCAAATCTATGTACACTTTCTCTCACATTTCTCAAGTGGACA GATTTCTGCATTATAGTCTGGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGTCTTT CCTACCCCTCTAAATGTATCTTNNCTAATTATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCCTTTGGGTGTTGTTGCTGTTGTTTCTCTGTAAAGNTGTTT
WI-1307	118 T C ---			GACAAGGCTGGTACTAGTTTCCAAATCCAAATCTATGTACACTTTCTCTCACATTTCTCAAGTGGACA GATTTCTGCATTATAGTCTGGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGTCTTT CCTACCCCTCTAAATGTATCTTNNCTAATTATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCCTTTGGGTGTTGTTGCTGTTGTTTCTCTGTAAAGNTGTTT
WI-1325b	169 T C ---			GAGAGATGGCCAAAGACAAGCAGAGGGAGAGAGAGCAACNTCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATTAGGCAACTACAATGTGCTTTGCTCTCTT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGT
WI-1325	165 C T ---			GAGAGATGGCCAAAGACAAGCAGAGGGAGAGAGAGCAACNTCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATTAGGCAACTACAATGTGCTTTGCTCTCTT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGT
WI-1327b	162 T C ---			CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGAAGAGTCTGTATTGTAAA ACACCAAGTGCGGTTTAAATGGAATGCGTATGTGTAGTNCATATTACGACAGGGCTGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGT/CJGAAGTTGGGTAGTACCAGGCTCCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTCTACTGAAGAGGCAATGGTTCATCTCTAAG
WI-1327	175 C G ---			CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGAAGAGTCTGTATTGTAAA ACACCAAGTGCGGTTTAAATGGAATGCGTATGTGTAGTNCATATTACGACAGGGCTGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGT/CJGTACCAGGCTCCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTCTACTGAAGAGGCAATGGTTCATCTCTAAG

WI-1341b	136	GA	---			TATCAGCATGATTGTGGCTGTTGGACACAAAGTCAATTTGTACATTTTGNNGNNNTCCTTTCTTTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAATTTGGCTTNCCTTTGTNTAAATATACCCCAAGC [G]AGGATTGTGATGGATCTGTTATTTCTGTCTTGGAACAGCAGAGCTGCTCTGNGAGTNG GTTTCAGGATTGTCTCTGTTTCCCGAGCCACTTGCACATTAGCAAGTGT
WI-1349e	192	GC	---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATA
WI-1349d	264	CA	---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATGAT
WI-1349c	192	GC	---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATA
WI-1349b	264	CA	---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATGAT
WI-1349	264	CA	---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATGAT
WI-1403b	57	CT	---			TGGTATTGGAATGGGTTACAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTGCTTTCGGAAT GCCACTTTATAAGTTAGAGGTATTACCTTTGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATCTTGGCCCTGCATCATGCAITTTGGCAATATGTCACATAGCTGTCTCA TAATCCCAAGTGCCAAAAAGGGTTGATCTGATTGT
WI-1403	58	T C	---			TGGTATTGGAATGGGTTACAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTGCTTTCGGAAT TGCCACTTTATAAGTTAGAGGTATTACCTTTGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATCTTGGCCCTGCATCATGCAITTTGGCAATATGTCACATAGCTGTCTC ATAATCCCAAGTGCCAAAAAGGGTTGATCTGATTGT

WI-1417c	31 C T ---			CAGGCCGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGGGGCGAGATGTGAGCCCCACGGG GGTGACAGCATGCCCTGCTGGCAATTTGGAGGGCCCCAGAAAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCTCGACTTCGGAAGTTAAGGGGCTCGGCTTCAAAAAGCTGGGTCCGGTTTGGAGCGGTTGC AGGCGAGGCCCTTAGGTCGGTATTTAATGTTTGGTTTGTAGAAAAAGTCGC
WI-1417b	31 C T ---			CAGGCCGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGGGGCGAGATGTGAGCCCCACGGG GGTGACAGCATGCCCTGCTGGCAATTTGGAGGGCCCCAGAAAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCTCGACTTCGGAAGTTAAGGGGCTCGGCTTCAAAAAGCTGGGTCCGGTTTGGAGCGGTTGC AGGCGAGGCCCTTAGGTCGGTATTTAATGTTTGGTTTGTAGAAAAAGTCGC
WI-1729	172 A ---			CCATGAGCAAAACAGCATGTTTCTACTCTGTGATGTGTATGTTAGGGGGCATGTATATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAAGA TGTTGGAGAACTGAAAAGAGAGCTTACATGCACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGATGTGTCCTTCGGTGGTNACCTTCTCCTCCACCACATCACCTGTGTTTTT
WI-1732b	122 T C ---			TGCCCTACTCTTTGTTCAATCCACCATTACATTTTGTAAATTTGGAATTTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAGGAGTNTCCCTGGTCAACCTTTT/CJATTGAGTCT CTGCCACATGTCTAGTAAGTGTGATGGTGCATGATATACTCGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATATATTGGCTAAGGTATTCATCATATATTGGCTAAG
WI-1732	114 C T ---			TGCCCTACTCTTTGTTCAATCCACCATTACATTTTGTAAATTTGGAATTTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAGGAGTNTCCCTGGTTC/TAACCCCTTTTATTGAGTCT CTGCCACATGTCTAGTAAGTGTGATGGTGCATGATATACTCGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTGGCTAAGGTATTCATCATATATTGGCTAAG
WI-1750	97 A G ---			GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTCCCCCAAAAAAGGTTTTAAATCTGTGTTGGA CATAATGTTGAATTTGAGTTTCACTTACCTTGG/AGTTTAAAGGTGTGCTTTTCTGGCAAAAGAGTCAG TGGAGTGTCCGGGAAAGGGCTAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCTGACTGAG CTACATTCACCTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---			GGTACACAAAGAAATGCTTCTGGAAATCTAC/AGTGGCCCTTAACATTTTGGCTGAGTATTAATC TGTACATGTGTAAATGTGAACCCACCATGAAGCTGGGCAAGAACAAATTCCTAGGAAAGTACAATTAC TGGGAAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGGAATCACTCATGTTCOCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAGGAATAATCATAAAAAT
WI-1803c	77 A G ---			CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTTCAGGCGAGAA CCATTATGAT/AGTGTAGGTAGAGCATCACACTTGGGAGGACATATTCGGAGTNAGATATCCTG GGTGTAAATTTCAATATATCTACTAAAGCATGACTTCTAGAAAATTAATTTACTTACTTCTGTCTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAATAACTGGAATCA

WI-1803b	77 A G ---	---	---	CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGATAGAGTAGGGTAGAGCATCACACTTGGGAGGACATATTCGTGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGCTCCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA
WI-1837b	112 C T ---	---	---	TTTACTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC[CTGCTGCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACTGGGAAGTCTGGGGAACGTTTAGCTTCTGCTGGCT
WI-1837	112 C T ---	---	---	TTTACTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC[CTGCTGCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACTGGGAAGTCTGGGGAACGTTTAGCTTCTGCTGGCT
WI-1840b	79 G T ---	---	---	TCACCTAGGGAGGTGCTAAAATGTAGCTTCATTAAAGACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT[G]GAGAATCTGAATATTCAGCACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTTCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	---	TCACCTAGGGAGGTGCTAAAATGTAGCTTCATTAAAGACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT[G]GAGAATCTGAATATTCAGCACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTTCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1879b	110 C T ---	---	---	GGGCTCACTTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTTTTCATAACTTACTCCCGG CACTGTAGGNTTTCTTTGAGGTNAAGGACCTGCCNTTTTAC[CTGCTGCNAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGACCCCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT
WI-1879	110 C T ---	---	---	GGGCTCACTTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTTTTCATAACTTACTCCCGG CACTGTAGGNTTTCTTTGAGGTNAAGGACCTGCCNTTTTAC[CTGCTGCNAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGACCCCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT
WI-1900b	119 C T ---	---	---	TGTTCTGTGTCAGGCACCGGCTAAGTCTTGTCTGATATGGAATAATCAACTGGACAACCCNG CTNAGGTAGNTACCTNGGCAATTAGCCCCCTTACAGCTGCAAAAGAGG[CTGCTCTGAGAGGT AAAGTCCCTGCCCAACGGGCAACTAGAGAGAGCAACAGGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAAGTGCAATGAGAAACCACTTTCTTTGCTCC



WI-1900	119	C T ---	---	---	TGTTCTGTGTCAGGCACCGGCTAAGTCTTGCTGCATAATGGAATAATCAACTGGACAACCCCNCG CTNAGGTAGGNTACCTNAGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTCCCTGCCCAACCGGCACAACTAGAGAGGACCAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAAGTCCCATGAGAAACCACTTTCTTTGCTCC
WI-1943c	165	C T ---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAGACCAAGC[C/T]CTCTGAANCTGGTCCACGTCGAGATAGTGAA TACAGGGCACCCGNTGAGCATTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165	C T ---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAGACCAAGC[C/T]CTCTGAANCTGGTCCACGTCGAGATAGTGAA TACAGGGCACCCGNTGAGCATTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164	C T ---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAGACCAAGC[C/T]CTCTGAANCTGGTCCACGTCGAGATAGTGAA TACAGGGCACCCGNTGAGCATTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270	A T ---	---	---	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTTGGAGTGAGGATTCGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACCTTAAAAATGCACCTCCCAACTTT
WI-1960b	270	A T ---	---	---	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTTGGAGTGAGGATTCGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACCTTAAAAATGCACCTCCCAACTTT
WI-1977	203	T C ---	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGATCA TTCTGGGCATTCTTCATAGAGTNTGTTTTTAGTCTCGTAATAACTGTGCCCTAGGAAGGTTGTT TTTCTACTGCGTCTGTGAAAGCCTTCCCATCGAGTGATACAGTACTTCCAGTTATGGAGATTTT /C]TAACAATCAAACTGAGGCTGAGGCTGTTGG
WI-2012	102	T C ---	---	---	AAATTCAGAAGCCAGAAGTCAGCTCAGGATTTATAAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATCTGCACAAAACCTAGCTAAAAATC[T/C]TTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAGCACTCAAAAGTTATGTAGAGTAGCTGTCTGAGTCACTTTTCTACTCTCATT GGCTTACCAATGCTTCCACTGGATC

WI-2013	127 C T	---	---	CTTTAGAGGTGGTCATTTGGTTCCTTCTGGAAAGTGATTGGTGTAAAGAAAAATAGATGCAACG TTGCTAAGTAGACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACTGACACTTC/TTCTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACITTTTTCAGTTATGCTCCCGGGTCC CCTTTCACTGGAGGATATCTAGCTTTCTGAGCCCTGGTTACTGCAATCC
WI-2032c	166 G A	---	---	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTTACTCATATAATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACAC[G/AJTGTTGGACCTCTGTCTCAACCTCCGACTTTTCAC AGATCATTTGGTTAGGCTCACCTTCTCTGTAATTGCTCTCTGTTTTCAAAGGG
WI-2032b	219 C G	---	---	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTTACTCATATAATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACGTGTTGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTTGGTTAGGCTCA/C/GTCTTCTCTGTAATTGCTCTCTGTTTTCAAAGGG
WI-2032	219 C G	---	---	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTTACTCATATAATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACGTGTTGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTTGGTTAGGCTCA/C/GTCTTCTCTGTAATTGCTCTCTGTTTTCAAAGGG
WI-2054b	188 C T	---	---	CGTTTTCTCTACATCTTTGGGNACATAAAGANGAAAGAGNAGCTGCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCAATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTTC/C/TTCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
WI-2054	183 T C	---	---	CGTTTTCTCTACATCTTTGGGNACATAAAGANGAAAGAGNAGCTGCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCAATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTTC/C/TTCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
WI-2573d	129 T C	---	---	TGGGATTAACACCCGTTTTCTTCTCTCCAGTTCAGTGGCTTAATGTTTGTGTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTCAAGGTGTTCCGGTCTTTC/TTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAGGGGTAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAAAGTCAATGCTGGGCTTGGACGAG
WI-2573c	165 A C	---	---	TGGGATTAACACCCGTTTTCTTCTCTCCAGTTCAGTGGCTTAATGTTTGTGTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTCAAGGTGTTCCGGTCTTTC/TTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAGGGGTAGCAACAGAGGCTGTGT TGAAGTGAATGATTGCTTGCACAAAGTCAATGCTGGGCTTGGACGAG

WI-2573d	129	T C ---	---	TGGGATTAAACCCCTGTTTCTTCCTCCAGTTCAGTGGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTTTCCGTTGCTTT/CJTGA TATCATCTGATCTCCCAACCAGGGCTTATTTATGCTAGGTAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAGGTCATATGGCTGGCTTGGACGAG
WI-2573c	165	A C ---	---	TGGGATTAAACCCCTGTTTCTTCCTCCAGTTCAGTGGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTTTCCGTTGCTTTTATGATAT CATCTGATCTTCCCAACCAGGGCTTATTTA/CJTGCCTAGGTAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCACAGGTCATATGGCTGGCTTGGACGAG
WI-2573b	165	A C ---	---	TGGGATTAAACCCCTGTTTCTTCCTCCAGTTCAGTGGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTTTCCGTTGCTTTTATGATAT CATCTGATCTTCCCAACCAGGGCTTATTTA/CJTGCCTAGGTAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCACAGGTCATATGGCTGGCTTGGACGAG
WI-2573a	129	T C ---	---	TGGGATTAAACCCCTGTTTCTTCCTCCAGTTCAGTGGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTTTCCGTTGCTTT/CJTGA TATCATCTGATCTCCCAACCAGGGCTTATTTATGCTAGGTAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAGGTCATATGGCTGGCTTGGACGAG
WI-2868b	60	A G ---	---	GACTTCATGCTCATGAACAAGCATTGTCTTAATTTACAGACATTAGAACAAGCTTTCC/A/GJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTCATCCACTTTAAAGAGGTTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAACGCTTCCCAATGATGCAGCCCAAGTTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60	A G ---	---	GACTTCATGCTCATGAACAAGCATTGTCTTAATTTACAGACATTAGAACAAGCTTTCC/A/GJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTCATCCACTTTAAAGAGGTTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAACGCTTCCCAATGATGCAGCCCAAGTTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131	T C ---	---	CATGCTGTGTAACTCTGTGCTGCTTGTGCTGGGGAATTAGAGCAAGGAATTGTATATCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAGATGAACATCAGGAAATGACTGGATAATGA/T/CJ AGAAATGAATAGAGCCCATTTTAAATTTATATCACAGCTTTATGTCCACTTCTGTTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT
WI-2870	131	T C ---	---	CATGCTGTGTAACTCTGTGCTGCTTGTGCTGGGGAATTAGAGCAAGGAATTGTATATCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAGATGAACATCAGGAAATGACTGGATAATGA/T/CJ AGAAATGAATAGAGCCCATTTTAAATTTATATCACAGCTTTATGTCCACTTCTGTTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT

WI-2954c	49 T A ---	---	TTAGCACATATCTGTGTGGGACTTAACCTGAGACAAAGGATAAAAAAT/AJAGCACCTCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	TTAGCACATATCTGTGTGGGACTTAACCTGAGACAAAGGCA/GJTAAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	TTAGCACATATCTGTGTGGGACTTAACCTGAGACAA/GJTGCATAAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/CJG CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGAACCTCCTCTCTTCAATAAACCTAAG ATTTCCCTTTGTTCCCTGACATCTGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTCTTTAATGTTATCTGAAAGAAACCTTTTACTTAGGGATTGTC
WI-2971	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/CJG CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGAACCTCCTCTCTTCAATAAACCTAAG ATTTCCCTTTGTTCCCTGACATCTGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTCTTTAATGTTATCTGAAAGAAACCTTTTACTTAGGGATTGTC
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTTGTCTCTGACTACATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTIA /TAAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTTGTCTCTGACTACATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTIA AATCTTTCTTTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTTGTCTCTGACTACATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTIA /TAAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151	G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAAGTAGCAGAAAGTGTT
WI-2995d	133	A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAAGTAGCAGAAAGTGTT
WI-2995c	151	G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAAGTAGCAGAAAGTGTT
WI-2995b	151	G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAAGTAGCAGAAAGTGTT
WI-2995a	133	A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAAGTAGCAGAAAGTGTT
WI-3147	85	C T ---	---	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCCAC ATCTCACTTAGCTCCTTC/TCCCTGCCATATCCTGTTTCCCTTACTCTCTATCTCTGAGACTTCTCCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTTNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCATAATCTTTGCAAGG
WI-3234b	68	T C ---	---	---	ATTCTGAATGTTTTCAGTCTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA T/C]GACAAAGCAAGAACACACAGAAAGCCCTGTTTGCAATCTGGCCCTTTATAAATACCTTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAAATGGAATGTACTTATTTTATCTTAT
WI-3234	68	T C ---	---	---	ATTCTGAATGTTTTCAGTCTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA T/C]GACAAAGCAAGAACACACAGAAAGCCCTGTTTGCAATCTGGCCCTTTATAAATACCTTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAAATGGAATGTACTTATTTTATCTTAT

WI-3292b	106 GA ---	---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTGATGGTATGGATGGGATGGATTACTT GCCATGAATATTTTCCATTGTTCTCATTAAATGATTAATTAATTAAGTAAATATATTNNCCATGA GACAAATGGAAAAATGGAAACATTCATGGAAAAAAACCCATTCAATC
WI-3292	106 GA ---	---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTGATGGTATGGATGGGATGGATTACTT GCCATGAATATTTTCCATTGTTCTCATTAAATGATTAATTAATTAAGTAAATATATTNNCCATGA GACAAATGGAAAAATGGAAACATTCATGGAAAAAAACCCATTCAATC
WI-3355	199 GC ---	---	---	CCATGAACCATGGGCTACA/GCJATATTCCTAAACTCAGAGTCCCTTACTGGAGAGGGATCCA CTTTTAAATATGATTTCTGAAGTGGCTGCATATTCCTCCAGCAGCTTAAACTCATCAGAA AAAAAATCATCAAAAGTCGAAGTTAGTTTATTACCTTCCACTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTINAGTTG
WI-3408	194 GA ---	---	---	CCATGAAGAATGAGTTCCCTCCCTCCCTGGGTGAGTCTAAGAATAGCACACCCCTTGAGAAATTTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCCTCCGCTAAGACACACCTTTATGCTTTTCAAGCTTT CTGGAATGGGATGAATCINACATTCATGTCACCTTCGTGTGGGATCACTTCTCC[G/A]TGCCCC ATCTCTGNAGAAGCCACTGGGAAGTCGAAGGAGTCAATCAATCAGG
WI-3505b	131 GA ---	---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAATTTT GAAAAATGGCAATTTTAAATATCTTTGGAAGTTCTTAACACATTAACCTATTTTNAACCAAAAC[G/A] AGGTATTCCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTTGCATAT
WI-3505	131 GA ---	---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAATTTT GAAAAATGGCAATTTTAAATATCTTTGGAAGTTCTTAACACATTAACCTATTTTNAACCAAAAC[G/A] AGGTATTCCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTTGCATAT
WI-3564b	177 CT ---	---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACTAAATGTTTGGAAAAATAAAGT GAAATCAATGTGCTTCCAGTGATTCACATGGCAGAGTGCACAGAGGCTTGAGCGCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTTCTTACAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCTTACAAAAACAAA
WI-3564	177 CT ---	---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACTAAATGTTTGGAAAAATAAAGT GAAATCAATGTGCTTCCAGTGATTCACATGGCAGAGTGCACAGAGGCTTGAGCGCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTTCTTACAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCTTACAAAAACAAA



WI-4110	130 T C ---			GAAATGATGTTTTGATTTCCCTTCTCTATCTTCAGATTATTGGAGTGTCTATTAGAAAACTGATAGT AACCTTTATTTGATGAACTCTGTCTATAATTAACCTTCTCTCTCTTTATTTTGGCTT/CJACA GTTTAGGTAAATAAAGATGCCAAGAATTCAGTATTCAAGTACAGTAAAAAGTAGCAACCATGGG GTAGGACAAGTNCAGAAAAAGGAGGAGGTTGGGGGTTTCTGGGAAGA
WI-4119b	168 G A ---			ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGCTTGGGTGGAAAAAGTAAATAAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGACAGAACAGACAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4119	168 G A ---			ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGCTTGGGTGGAAAAAGTAAATAAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGACAGAACAGACAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4123b	51 T G ---			CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAAAAATAGAAAAAGTG[T/G]TTTAACTATTT CAAATAACAATAAAGAAAAACATGATGAAATTTCTCGTTACATAATTTGATAGAAATTTAGTGGGG TTCTTCCATGACATTTGGCTTGTCTTCTCAACAGTGGGTGGTTGGATGTTTTCTATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51 T G ---			CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAAAAATAGAAAAAGTG[T/G]TTTAACTATTT CAAATAACAATAAAGAAAAACATGATGAAATTTCTCGTTACATAATTTGATAGAAATTTAGTGGGG TTCTTCCATGACATTTGGCTTGTCTTCTCAACAGTGGGTGGTTGGATGTTTTCTATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145 G C ---			TTGTACATGTTCAATTCATCCCTCCCATTTCTTTCTGTCTTATAAGAACCTCGCTTCTTCCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTTATTTCCATCAAAGCTTCTCAGCATCTTCTATATACT GTGCTGT[G/C]CCTTGTGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGTTGAACGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATG
WI-4149a	137 T C ---			TTGTACATGTTCAATTCATCCCTCCCATTTCTTTCTGTCTTATAAGAACCTCGCTTCTTCCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTTATTTCCATCAAAGCTTCTCAGCATCTTCTATATACI T/CJGTGCTGTGCTTGTGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGTTGAACGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATG
WI-4182	188 G A ---			TAACACACTTTTCATTTGGTTTCTTATTAAGTGCAGTTAAAGGACCATCCATTATATTACAATTCCTC AGTTCTATGCTTTAGAGTNCATTAATAGGACTACTGTAAAAATTCAGAGGGAATTAATCTCTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTCAGGGGACTGTGGTTAA[G/A]ATGTCTCTCT TGCCCCCTTCCCAAGTTCTTAAATTCCTAG



WI-4230	93 T ---				AGAGACGTTGAATGGGGACATCTTTCTATTTCGATTTTAGTTTAACATTTGATAAGAATTGATGAAA GTTTGTACATTCAGATTATCTTTATAGCAGCAGAAGTCTGGCAAATAATAACAGCACACTGACT TTTCCATGGTAAAGAAAGTTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAT ACATTTAAATGGAGGAGATGAATAGTGACCTTTGAAATTTTGAATTTATGG
WI-4241	118 CT ---				GAAATTCATTGAAGTTTGAACCTTGAACCTGATCTCATTAATACCTTTTNCCTGAGGTTGATTT CATTTTGACAACAGAACAGACGAAAAATTTCCACTTAAATTAATTCCTC/TJAAGTATCTATGAT TTAGCACTGTTAGCACCAGAACTGTGAAATTTATCTCTAGATATCTTCAGAACTCTAGGATGGAAG AA
WI-4271b	151 A ---				CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGAGCCCCAACCCCTCCCCCTTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A ---				CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGAGCCCCAACCCCTCCCCCTTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 GA ---				AATCGAAACATTTGATTTTGTAAAGGAACCATTTATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATGCTAACCTTTTGGGA AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAAGTGAAGCGGTAA
WI-4389	156 GA ---				AATCGAAACATTTGATTTTGTAAAGGAACCATTTATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATGCTAACCTTTTGGGA AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAAGTGAAGCGGTAA
WI-4488	31 A G ---				GATGACAATTATTGTGATTGGCATTTTAA[G/G]GTACCATTCATTTTCTTCTGGCTTTCGTGTGTT TGTTGTTGAGAAGTCAGGGGTTAGTCGATTGCTCTTTCTAGTCTCTCAGTAGGAAGACTGATC CTAAACAACTTAATACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAAATCAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 GC ---				ACCATCAATGTATCACCTTCTAAATTTATTAGATGATTAACTGGCTCTGTTAAAAATAAAAACCT GTCTTGACATTGAAAAATAAACATTACTATTGGTCATTTTCTGCTACTACAAAGGTACTGCACCTA AACAAGTTAAG[G/C]GTTTGTGGAGGGGAAAAATCATAAAAATGCATAAAAAATTTCTACCACGTCA TTTCTTGTCCCATAAATAAAATTTTACATGCCT

WI-4584	144	A G ---	---	TTGGTTGGCATTATAGCCCTCATAACAACATATTACAATCATAAATTGTTACTCTTATTTTACAAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGAGAGCCCAAGATTTGAACCCAGGAATCCATT CACCGGTACAGJTGCTACCTGGGTAAAAAATGTTTAAATAAAATCTATGGCATTAGATTTCAAAGA GTCCTAATGGTTTGAATAAGGTGCTTTAATTTGTTTATCAGTATGC
WI-4639	185	C T ---	---	TTTCTGCAATTTGAATGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAAATCCACCATTTAC TGACCATATGACTTGGGGAACATTTATCTCACCTATCTGAGTGTGTATCCCTCATCTTTAAATTTGTA AATTTTAAGGACACCTATCATAGTAATAATTGTGAGGATAAAATGAAATAA
WI-5327	63	A ---	---	AAATGAATCCGCTTTAGAGCAAAATACCAGTAAGGGCTGGTGCAGGATGGTGGCTGAGAGAJA-- JGATTACTCATAAAAGCATATTAAATTTATAAAATATGAAAAATTTAACTAGATAATTAATGTGAAT TGAGTTGAAGGTTGCATGAGAGTAGGGAGGAGGTAGTTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAAATGGCTCTTTCGGATGACAATGATGAACCTGTTCTAAGCAGACAG
WI-5390	87	C T ---	---	GCCTTTGAGAAATGAAAAGGGAGCCTGGACCATTCAGGGCTCTCTCACTCTGATATTTTGTGTAT TTATTGTTCACTTATTATTC/TGTCTCTCCCTTCTGGTATGCTTGTCATGAACAATGAATTC CCAGTGGCTGGCCCGAATTCGTGGCTCCTAGAGGTGCCAGAAAAAAGTTTCGGTGAATAGAAATTG ACGAATGGGTTCAGAAATGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATTTATTTAAATTTG/JAAAGAAACTTGTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTTATAACAA
WI-5404	87	G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATTTATTTAAATTTG/JAAAGAAACTTGTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTTATAACAA
WI-5545b	77	A C ---	---	TAGGAAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTTACCACCTCACACTGCCGCCA TATCTCCTC/JCJCCAACACCTCTGTTTCTGACAGCCCAAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCAATTTCA
WI-5545	77	A C ---	---	TAGGAAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTTACCACCTCACACTGCCGCCA TATCTCCTC/JCJCCAACACCTCTGTTTCTGACAGCCCAAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCAATTTCA

WI-5860b	134	A G ---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTCTGTAAGATTTTATTTGT TTCTTTTATATAAAATATGGAATTTGTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACACTAC/A GJTATACCTGGAATCATGTGAAGACATTTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-5860	134	A G ---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTCTGTAAGATTTTATTTGT TTCTTTTATATAAAATATGGAATTTGTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACACTAC/A GJTATACCTGGAATCATGTGAAGACATTTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-6106	208	C G ---	---	GCAACAACCTATTATACCTGATTCOAACCCAGGTCTACTAATTAATCAACCCCTAACCAATAC TATATATTGCTCTGTTCTGAATTAATTTTCAATTTAGAACTGTAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATTTCTTACAGAG TAATTC/GJATAGTAGGTACCCACAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTTC/CJ AAACCCCTATATTNCTGTCCTTGTGCATACCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATGT GNAAAATTATCCCTGAAATTTTATACCA
WI-6109c	147	T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTTAA ACCCTATATTNCTGTC/CJCTTGTGCATACCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATG TGNAAATTATCCCTGAAATTTTATACCA
WI-6109b	147	T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTTAA ACCCTATATTNCTGTC/CJCTTGTGCATACCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATG TGNAAATTATCCCTGAAATTTTATACCA
WI-6109a	129	T C ---	---	AATGCCCTATCACCTTCCATCATGCTGCATACTGATTGATTCATTAATGCTTATTGTTAGCACCTGTC TTCCAACACATGCTGTTTTGTTCAATGATTC/CJGCATATCCCAAGTGCCTTAGACAATGCCCTCCCATAC AGTGAACAGTATTGACTAAACATACCTTGTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC
WI-6112	96	T C ---	---	

WI-6244	103	C T	---	---	---	TAATTGCACAACTTACATATCAGGGTTCTGATTGAAAGGAGAGAAATATTCCTTTCTTTTAGTGATT GCTTAATATTAAATCAATAAAGTGACCAATCTCTT/CJGCTCCTTATAAATGTGTTTAGAAGAAGG AAATTGAGTGTGGGAATTAAACAACAGGAGACATTTTATATCTCTACAGTGGGGAAGACTT CCTATTCTTTCCCAAGGATGGATACATTTCTAC
WI-6268	124	C T	---	---	---	CTGGCCTTATAATCCAAGTTTAGGATTAACTTACCCCACTTAATAGACTCCAGACAGTTGCAGTT GTCTACAAGATTTCTCTCTAGTAGGGCTTTGGGTGTGGCACCCTTTGGCTCATTC/CJACTCTCCCT GGGTCTTATTGACTTTGAGGGAGCCTAGAAAGAGCTGGACAAAACCTGCTCTTTGCAGAAAGAGTCG GGGTCCAAAGATTTCGTTACGATTTTATA
WI-6336b	234	C T	---	---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCCC ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAACTAATTAAACAACATAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTACAGATTAATAGATCACATGAAATGGACCATGTG GTACCCCAAGTGCATTATGCTTGGTAGAGCC/CJTTGAGGACACTGACAGT
WI-6336	234	C T	---	---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCCC ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAACTAATTAAACAACATAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTACAGATTAATAGATCACATGAAATGGACCATGTG GTACCCCAAGTGCATTATGCTTGGTAGAGCC/CJTTGAGGACACTGACAGT
WI-6381	92	C A	---	---	---	TTGGATACAAAATTGAGTTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAAATTA CAAAAATGNNTCATGTTTAAACA/CJAGTATTTTAAAGCTCAAAACATTTTAAACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGCTTTTGAATGTCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTCAG
WI-6436	198	C G	---	---	---	GGTTGAGGCATTGGGAAAGGCAGAAATTTGAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAAAGTCATGACAGACAGGAAATACAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTTGGTGTCAATAAAGAAATTTAGACITTTGGTGTGTAGTAGTTGATAGTAGGTAGCGTT/CJ GJATTGGGTGATTCCACAGACAAGGTGATGTTCTAAGATTTGATATTTATTGT
WI-6449	186	C T	---	---	---	GAGGCCTCTTTGCTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGCTGATTGGTGGTGTCTCAGCTCAGCTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTCTATTCACTGCACTCTCTGATCTATGCTGGCTCTATT/CJATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTCCCTAAATTTTCTGTGGGTGATTTATA
WI-6449	186	C T	---	---	---	GAGGCCTCTTTGCTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGCTGATTGGTGGTGTCTCAGCTCAGCTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTCTATTCACTGCACTCTCTGATCTATGCTGGCTCTATT/CJATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTCCCTAAATTTTCTGTGGGTGATTTATA

WI-6463	72 T C ---	---	GCTGGAGAGAAAAGACCTCCAAAAGAAAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACATTC/TGAAAAAAATTAAGTAGAACTCAAGAGAGCCAAAAGTCCCAATTGTGTCATT TAAGAAATATTTGAATGGAAATCTTAAGAATGATTTTATGATCAGTTAAATGTTCTTCCTCCTC CAGTCCCATTTATATGACATTCGGCATGCTG
WI-6474b	76 C T ---	---	AAGCAGTAAATCTTCCATCGCATGGATGCCAGTGGGTAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA/C/TGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAAGGGGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---	---	AAGCAGTAAATCTTCCATCGCATGGATGCCAGTGGGTAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA/C/TGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAAGGGGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---	---	GAACTCAATTAACTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCAGCTTCGAGGCCGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGAGAAATCAGAGT/A/GCTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---	GAACTCAATTAACTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCAGCTTCGAGGCCGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGAGAAATCAGAGT/A/GCTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---	CACATTTGAAATGCAACTGAGAAANTGGTTTNTAGGCCCTACCTTTTATTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATTTCTGATCATTTTATAGNTCCCAAGCCCA TTAGCAATATCTTA/G/ATCAAAATTTTAAAAAGAGAACAGGAAATAAGGAAGGCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCCTATGC/G/ACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCCTCATTTNCTCAGAAATGGAAGCAATTTGATTATNATTTTTTTGGGTCTGTGTAAG GTTCC/TGGCAGGAGAACATGCATATGACTTTTAAATAAGACCAACA
WI-6564	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCCTATGC/G/ACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCCTCATTTNCTCAGAAATGGAAGCAATTTGATTATNATTTTTTTGGGTCTGTGTAAG GTTCC/TGGCAGGAGAACATGCATATGACTTTTAAATAAGACCAACA

WI-6608b	46 C ---	---	CTAATCAGTAGCACTGAACATGGCTCTAGTGGGCTCAGT[C/- JAGTTAGGCAGCTAAGGAGGGGATTTCTCTAGCTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTCCAGCACTAG GTAAACTGCAAAAGAAAAACACCTGTGCCAGGCACCTAGCTACAAGGCCACACCAGAAAAAGGAA AGC
WI-6608	46 C ---	---	CTAATCAGTAGCACTGAACATGGCTCTAGTGGGCTCAGT[C/- JAGTTAGGCAGCTAAGGAGGGGATTTCTCTAGCTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTCCAGCACTAG GTAAACTGCAAAAGAAAAACACCTGTGCCAGGCACCTAGCTACAAGGCCACACCAGAAAAAGGAA AGC
WI-6666	68 C A ---	---	GTAGACAGTATCCAGCAAAAAAGGTTATTTATACCTCTACTTTCCAAAACGAGGAAACCTCCCC A/C/AJAAATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGTCTACTCTGTTGGTTTCATGTAA ATGTTGGGGTGACTCATTCGGCTCTTCNTTCTCAAGTCCAGGCTCTTGGGTAGACCAAAAACTA ATACACAATGTTAGAGCACACAAGAGA
WI-6670b	120 A G ---	---	AGATTACATAATTACTGGGGCCATTGTAGGGTNGGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/A/GJTTGTAGCCA GCATTGCCATTAGGGCCGAGTCAGGGTTGTGGGCCAGAACTTAGACAATTTGGGGAATTTCTGA AAAAAAAAGAAATACAGAATTGTAAACACAGACACAGAACTTAGAAGGGAT
WI-6670	120 A G ---	---	AGATTACATAATTACTGGGGCCATTGTAGGGTNGGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/A/GJTTGTAGCCA GCATTGCCATTAGGGCCGAGTCAGGGTTGTGGGCCAGAACTTAGACAATTTGGGGAATTTCTGA AAAAAAAAGAAATACAGAATTGTAAACACAGACACAGAACTTAGAAGGGAT
WI-6704c	33 T C ---	---	TTTGAAAATAAATTCATGCACCAATGTTTAACT/CJACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTAAATATGTTGTACATGTCATCATTAATCGATTCAATGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T C ---	---	TTTGAAAATAAATTCATGCACCAATGTTTAACT/CJACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTAAATATGTTGTACATGTCATCATTAATCGATTCAATGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C ---	---	TTTGAAAATAAATTCATGCACCAATGTTTAACT/CJAACTCACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTAAATATGTTGTACATGTCATCATTAATCGATTCAATGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 GA ---	---	CCATGGACAGTTAATTAGGAAGCTTCGACCTGTTAGATAACAGAGGAAGTCCAGTTATCTACCT ATTCCTTAAACACACATTTTGTGAGGCTGGAATGATCCCG[G]ATAGTAAACACTCAACATCCACACCT GCATAACATCGCTCCCAAGTACTATTTACTGAGTCGACACAGGATGTCACCAGTGAGCCTC ATCTCCAGTCCAATGGAGGAGTTGACCTTAGACCTTCCTGGACAGGAAGGGTC
WI-6766b	148 GC ---	---	AAAACAAATGGTGCAATGCATAATATTTGTGGTCACAGTATAAACAAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTCTTTGTCTACGGAAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G]C/JAAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGGAGGGAACCTACCAATCCAGTCCCTCTTC
WI-6766	148 GC ---	---	AAAACAAATGGTGCAATGCATAATATTTGTGGTCACAGTATAAACAAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTCTTTGTCTACGGAAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G]C/JAAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGGAGGGAACCTACCAATCCAGTCCCTCTTC
WI-6787b	97 A G ---	---	ACAGATAAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTTCTTTACAGACTTTTTTTTATACA ATACCTGTGCAGCAATGTTCAAATTTTAC[G]TTTTACTGCATAAGATATCTTCATGTACAACTGT ATGCTTGTCTCTTGGGAAGGACGCGTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTGAATAGGGCAGAGTAGANTACTCACAGGAAAGAGTAAATTCAGGT
WI-6793	105 C G ---	---	GAACCCACAGGTCCTGTTATTTTAAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGCGGCTCTCAAATCAATCAGTCAACCCCG[G]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTTGGCTGTAGGAAGTAGGGTTAATGCCCTCTAATCCCGGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACAGTTTCTCATCACAGGTAAAAAGGCAAC
WI-6810b	37 T C ---	---	CACAATAATAAAATCACTCCCTACCTTGAANAACTTTAT[C]JAGAAAGCATTTTAAATTTACAACACA AAGCTCAACGNAACCTACAATAAGTCTAGTAGTCTGTTCACNGCCCAAGGGATAAGGCTGAACAATA AATTAACCTTTAAAAATGCTATGNACAAAGTACAATTTCTTTTGTAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ---	---	CACAATAATAAAATCACTCCCTACCTTGAANAACTTTAT[C]JAGAAAGCATTTTAAATTTACAACACA AAGCTCAACGNAACCTACAATAAGTCTAGTAGTCTGTTCACNGCCCAAGGGATAAGGCTGAACAATA AATTAACCTTTAAAAATGCTATGNACAAAGTACAATTTCTTTTGTAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C/A ---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACATGTAGCT GCAGGGTAAC[C]A/JGTGGATACCCCTGTGTGCTCTACTNGCCCTCCAAAGGCATTACGGGGATCATCA AAGATGTTGGACACCTTGTGTCAAATCTTGGTTCAAGTGGGCTGTGCG

WI-6817	145 C A ---	---	GCATGATTAACCAAGTGCAGAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C/A]GTGGATACCCCTGTGTCTTACTNGCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTTTCAATCTTGGTTCAGGTGCGGCTGTGCAG
WI-6819b	221 C ---	---	GATGGAAGCCATTTTATTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTAC CATATGTCAACCTGAATGCCAGCAATACCTCGACTTTACACACGCGAGGAGCCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTATGTGCTCTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTG CTTTAGCAAAACAGCAATAACTTTTGTGTTCCCTATATGACACCTTAATCCAG
WI-6819a	175 G T ---	---	GATGGAAGCCATTTTATTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTAC CATATGTCAACCTGAATGCCAGCAATACCTCGACTTTACACACGCGAGGAGCCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTATGTGCTCTCAACAGTTTTCATATACAAAATTTTCTGCTATTT TTGCTTTAGCAAAACAGCAATAACTTTTGTGTTCCCTATATGACACCTTAATAT
WI-6826b	154 A G ---	---	GCAAAAGCTTTATGGCTCCAAACAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTGACAT[C/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTCGAAATATGCAACACACACTGGAGTGGGTATACGTTG
WI-6826	154 A G ---	---	GCAAAAGCTTTATGGCTCCAAACAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTGACAT[C/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTCGAAATATGCAACACACACTGGAGTGGGTATACGTTG
WI-6857a	122 T C ---	---	AGTGCAAACTATTTGAACAAAAGTAAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAATAATTCACATAAGTAAATAACAGCAGATGAGATGTCTCACATGTAT[C]ATTTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTGAGTAAATTTCCACAATAATATAGCAGCTCA AACACAAATGCAGGAGCACAAATGGCAAAAGTTTGGCAACTGTTTGGGCTAATT
WI-6865	153 G A ---	---	TTATAGAATCTTATGGGCATACGNGTAAATGAACGTGCAACCTTAAATCTAAACAACAGCTTG TTTGTTGCTGCTGAAATCCTCCTGCTCACAACAGCCAGCTACTNGGTTTTCTAAAGACGTA ATTTGCAGGCAAACT[C/G]ATGAGCCATTCGTGCAGAAGAGGGAAGGAGGAGCTGTTGTT TTACCTGTAGTAGAATATCTTTGCGCTGTAGAACTGAGCTCATTA
WI-6909	73 C T ---	---	ATTGAAAACTGTTAGCAACAGATAAAATACAATAGAGCCTGGATATAAAATGAGAGAAGAAATGC AGACTTA[C/T]AAGCTTATAGAGAAAGTCAAAAGGAGCAAGTTTGAATCAGATTTTATGATAC GGAAAAAAATTTCCTTTTTGGCAACAGGATTATTCGAAATAAATAAATCTGCCAGTGCCAAATCAG AAACACCATTTCCACAATATTTGCATGCCCTAGTTGCTTATTTATACATATC



WI-6910b	163	G T ---	---	CACTCAAAACCTTTATTCAATTGATTACAAACTGTACAATATTTACAAAGTTTAGGCATTAAATCCCA TATTGACATGAATGCTGGAGAGTCTAAAATAAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAAGTCCCGGACCTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144	A ---	---	GCTTGTTTTTTTGTGTTTTTAAAGTGACACCTTGGCCTTGTGGCATTCTTCACATTATCTTACCC AAAAGTGCCTTTGGGCCAGCCACTGACTGATTTAAACCAGAAATGTGGTTTTAAACAATGTGGT CGTGGTGAATTCAGGTGATTTTNAATTTCTATTTGGTAGTATTTTCAGATTTCCACAAAAGACATG TATTGCTTTTGTAAATTTGAAAAAATAACAACAGGATAGTAAAGATAT
WI-6928b	175	T C ---	---	CAATCAAAAAGTCCAAGTTTCAAAGCTGGGATGAAAAGCCAGGCTCTCTGACTTGCACCTCTGTCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTCATGTCCCATG CTTTGCTTTGGTCCCTGTGAGGAAAGGGTCAGCTAAAGGTC/CAACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATAATTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175	T C ---	---	CAATCAAAAAGTCCAAGTTTCAAAGCTGGGATGAAAAGCCAGGCTCTCTGACTTGCACCTCTGTCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTCATGTCCCATG CTTTGCTTTGGTCCCTGTGAGGAAAGGGTCAGCTAAAGGTC/CAACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATAATTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79	G A ---	---	TTTTATGAACATTTCAAGTTCCTTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAATTCCTAGTAAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACATAGGTAGTATTAANCAAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAGC
WI-6955	79	G A ---	---	TTTTATGAACATTTCAAGTTCCTTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAATTCCTAGTAAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACATAGGTAGTATTAANCAAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAGC
WI-6957	47	C G ---	---	AAACTAAAACCCCTTATTGTCTCCAAGTGTGGCAAAATAGAAAATC/GTTCATTAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATCCACTTAAGAAGCATTCAGTCAATAATACAAAA ACAAATTCAGATTGCTTGGATCTGGTCATTTATGGCTGAAGAAGTGGATTTGAAAACCACTTTAGG CTAAAATAAATGTATGAATAATGCATAGACTGTGTATCTAGAAAATCATGC
WI-6996c	242	G T ---	---	ACTTCTAGTGCCTCTGTACCACACCTCTAATGCCCTCTGGTCCCGCACTCTGTATGTCGTAGGCCCT TAAATCTGCCTGGCGTCCCTCCCTCTGTCTTCAGACACCCAGAGGAGAGAGCCGGCAGTTCCTG CAGGAGAGAGGAGGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTCTGCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTCTCCG/GTTCGGATC

WI-6996b	242	G T	---	---	ACTTCTAGTGCCTCTGTACCAACACCTCTAATGCCTCTGGTCCGCGCACCTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGTCTCAGCACCCAGAGGAGAGAGCGCGGAGTTCCCTG CAGGAGAGAGGAGGCTGTGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCTCTGACT CTCTCCTGATGGTGGCCCTCTGTGCTCTCTCTCCG/GTGTCCGATC
WI-6996	228	T G	---	---	ACTTCTAGTGCCTCTGTACCAACACCTCTAATGCCTCTGGTCCGCGCACCTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGTCTCAGCACCCAGAGGAGAGAGCGCGGAGTTCCCTG CAGGAGAGAGGAGGCTGTGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCTCTGACT CTCTCCTGATGGTGGCCCTCTGT/GTGTCTCTCTCCGCGGATC
WI-7021b	112	G A	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAAT/GA/CCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAAATTAATCAAACC ACTGTTATTAAACAGATAATAGCAACTTGGGAATGCTTATGTTACAGGTTA
WI-7021	108	A G	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAAT/GA/CCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAAATTAATCAAACC ACTGTTATTAAACAGATAATAGCAACTTGGGAATGCTTATGTTACAGGTTA
WI-7056c	118	C T	---	---	GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCTCCACCTCACCCTCCATGACAGCGCTAAACGTTGGTGA/C/TTGGTGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAGTTTCCAAACAACAGAAAGTCATTCCTCTTTTAAA ATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7056b	118	C T	---	---	GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCTCCACCTCACCCTCCATGACAGCGCTAAACGTTGGTGA/C/TTGGTGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAGTTTCCAAACAACAGAAAGTCATTCCTCTTTTAAA ATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7091b	153	A C	---	---	AATTGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCTCTTCTAACATCTTAGAG GTCCATGGAGAAAGGCATATGGAGAACATGTTTTATCTGCTCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAATAGCATTT/C/TTCTTATCATTTATCAGCCTTTTATGTATTTTCCAAAGTAAATATTA ACATATTATTTCATTGGTCTCTTTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153	A C	---	---	AATTGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCTCTTCTAACATCTTAGAG GTCCATGGAGAAAGGCATATGGAGAACATGTTTTATCTGCTCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAATAGCATTT/C/TTCTTATCATTTATCAGCCTTTTATGTATTTTCCAAAGTAAATATTA ACATATTATTTCATTGGTCTCTTTTTTATCTGTTCTATATGAATGCTAT

WI-7136	58	T C ---	TGTGAAGCCACATTTTCCAACTGAGCCTCATGAAGCCAACTAAGTGTATTGAACGTGTC/CAATTC TCTCAATAACTCAGGTAGCACCTTTAAAGTCTGAAGGACACGACATCAATGAAAGCATATCAATGTG GTGGAGAAAGGGAAGGGTGGCTTTTAAATTTATTTTCTTCATCTTTTATAACAAGAAAGNNNN NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTAGCTTCTATATATG
WI-7146c	210	A G ---	GGGACGCCTGTTGTTTGGCTCAATTTGGGTTTGGTGCACATGGAGCTCTCCATTTGTTTACGTG AATAATGAGTTGTTCTAGAGGACAGCCTGTCTCCTTGTGGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGATGCC AACGC/A/GJTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146b	210	A G ---	GGGACGCCTGTTGTTTGGCTCAATTTGGGTTTGGTGCACATGGAGCTCTCCATTTGTTTACGTG AATAATGAGTTGTTCTAGAGGACAGCCTGTCTCCTTGTGGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGATGCC AACGC/A/GJTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146	202	G A ---	GGGACGCCTGTTGTTTGGCTCAATTTGGGTTTGGTGCACATGGAGCTCTCCATTTGTTTACGTG AATAATGAGTTGTTCTAGAGGACAGCCTGTCTCCTTGTGGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGATG/A JCCAACGCAGTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7153	161	A T ---	ATATTACAACCTGCTTTTAGCTGATCTCCATCCTCAAAATGACTCTTTTCTTTATATGTTAAACATA TATAAATGGCAACTGATAGTCAATTTGATTTTATTCAGGAACATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAAACNNNNNNN/A/JAAAAAAGTTATTTAACAGTAATCTATTTACTAATAT AGTACCTATCTTTAAAGTATAGTACATTTTACATATGTAATGGTATGTTT
WI-7155	156	T G ---	TAGAATAGATCGGTGTCATATCTCTTTGGCTCTGGTCTCCAGCCCTCATGGTTGGCATCACATAT GCCTGCATGCCATTAAACCCAGCTGGCCCTACCCCTATATGATCCTGTGCTCTAAATTAATACAC CAGTGGTTCCTCTCCCTGT/G/JTAAAGACTAATGCTCAGATGCTGTTACGGATATTTATATCTAG TCTACTCTCTGTGCCACCCCTCTCTCTCCCATCCCAACTCCAG
WI-7169b	161	A G ---	AGCTCCACCAGATGCAGATTTGTTTGTGTTTCTGTTATCTACTGTCCACAGCTTATAACATGTAT GCTTTTCAGAAATACAGTTGCTAGCCAAAGCCATCAAGTGTCTGAAATTCATATTTGGTTTATGCAAA ACAGCAAACTTTTATTTAAGTAGAT/A/GJGGAGAAATATGTTTAAAAATATTAGGAATCCTAGAACATA TTTTCAAGTCATCTTAGCAGCTAGGATCTCAAATGGAAGTGTATATATA
WI-7175b	194	C T ---	CTCTAGACTAGTGCTTTACCTTTATTAATGAACGTGTACAGGAAGCCCAAGGCAGTGTCTCTCACCA ATAACTTCAGAGAGTCAGTTGGAGAAAATGAAGAAAAGGTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGCTGTCAATGTCCATGCCTA/C/JTAGAT AATTTATTTGATTTTGAATAAAAAACATTTGTACATTCCTGATACTGGG

WI-7175	194 C T ---	---	---	CTCTAGACTAGTGCTTTACCTTTATTAATGAACGTGTACAGGAAGCCCAAGGCAGTGTTCCCTCACCA ATAACTTCAGAGAAAGTCAGTTGGAGAAAATGAAGAAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGTGTCATTGTCATGCCTA/C/TJAGAT AATTTATTTGTATTTTGAATAAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273 G A ---	---	---	TGTACAGGTCAGGGACTTGGACAGGAGTCAGTGCTGGCTTTTCCCTCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCACCTGGCTCCTAGGGGAACAGACCAGTGACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTCTGCCTAAGAGAAAATTCGACTAAATGAATCTCGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273 G A ---	---	---	TGTACAGGTCAGGGACTTGGACAGGAGTCAGTGCTGGCTTTTCCCTCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCACCTGGCTCCTAGGGGAACAGACCAGTGACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTCTGCCTAAGAGAAAATTCGACTAAATGAATCTCGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116 A C ---	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTACCACAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCTA/C/TCTCTCCTCTATTT TACTGAGGCTGCCAATACAGCCCCACGTTTCAGCTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTTCCCTGAAGCCTAGTACCCCAATT
WI-7182	106 C A ---	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTACCACAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCCA/C/ATCTGAGCCTATCTCTCCTCTATTT TACTGAGGCTGCCAATACAGCCCCACGTTTCAGCTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTTCCCTGAAGCCTAGTACCCCAATT
WI-7191b	273 T A ---	---	---	ATAATTGCTTGTCTAGCCTGGCAAGATATTTTCATAAAAGAGGATAACAATGCTGATTACTAC CTTTTAAATATTTTAGATAAATGCACAGCACCACAGCCACATCTAAGCATTAGTGATGGGTAGC TGATGTCAGCTTCATGTGGATTTAAGCAGCTCTAGAAACAATGAAGCTTCTGGCATAATTTAAGGAG CTCCCAAAATGTTACCTATTAAATTTGTAACCTCAGCAAGTAGAAGACCAATT
WI-7199c	112 T C ---	---	---	CCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCCTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT/C/JGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAAATAGCATTCTTAATGTTTGTGTTGTTGTTGTTGTTGTTGTTTCTTTTAT AGTCTATAGTTTACTCCTCAGTTCTCACCACATCATCTTGTCTAA
WI-7199b	112 T C ---	---	---	CCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCCTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT/C/JGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAAATAGCATTCTTAATGTTTGTGTTGTTGTTGTTGTTGTTTCTTTTAT AGTCTATAGTTTACTCCTCAGTTCTCACCACATCATCTTGTCTAA

WI-7216c	237	T C ---				TGACACTAACACTCTAATCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTCTCCCTCCGCAAAATACGATGT AAGGACAAAATGTAGAAAGATGTGAGATACTTACTCAAGATTCCCTCCAGAAAAATACGATGT TTAAAAACCCCTTCTGCTATACATAGGAAAGACACACATCCACCTAAAAATTGACTGTACTGTGTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTGTITTTTTCCTTGTAAATCACTT
WI-7216b	237	T C ---				TGACACTAACACTCTAATCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTCTCCCTCCGCAAAATACGATGT AAGGACAAAATGTAGAAAGATGTGAGATACTTACTCAAGATTCCCTCCAGAAAAATACGATGT TTAAAAACCCCTTCTGCTATACATAGGAAAGACACACATCCACCTAAAAATTGACTGTACTGTGTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTGTITTTTTCCTTGTAAATCACTT
WI-7220b	147	A T ---				AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTTTGTCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATTAATCTTGAGCACAGTGAATGACCTATCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTIT
WI-7220	140	A T ---				AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTTTGTCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATCTTGAGCACAGTGAATGACCTATCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTIT
WI-7226	232	C ---				GATCGAATTTTCAGATGATTCGGAAATTTTCATTACGGTATTTGTAATAGTGACATATATATGATA TACATATCACCTCTTCTTAAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTGTGATCATTT CCCTTTCCATATAGGAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTGAGTGAAATAA TTACCCACAAATGCCACCAGTAACCTTACGATTTCTCCTTGGGGTTT
WI-7228b	254	G A ---				ATAGCTCCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTTGGCTCCAATTCATAA TATGTTCAACGAGGATTAACAATTTTGTCTCTTGTCTTTGTATCTATTTAGTTGATTTTAAATTA CTTCTGAATAACGGAAGGATCAGAAGATATCTTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAATAAGAAATGTTATCCAACATTAAGATATCTCAATGT
WI-7228a	163	G A ---				ATAGCTCCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTTGGCTCCAATTCATAA TATGTTCAACGAGGATTAACAATTTTGTCTCTTGTCTTTGTATCTATTTAGTTGATTTTAAATTA CTTCTGAATAACGGAAGGATCAGAAGATATCTTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTAAATAAGAAATGTTATCCAACATTAAGATATCTCAA
WI-7233c	213	C T ---				CGATCGTACTGCCAGTAGCATTTGCTGTCTGTCGGCTTGTGTTGTACATTCATTTCAATTGTTACA GATGTGAACCTTATTCCTTGTCACTAAATTAATTAATTAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTAGCCCTCTACTTCTTCTGCCACCCTTTTGTGGCAATATTAAAGTGAACCTGCTAATA GTGTAAGTATCTGTGCAACAAACCACTGCCAGATAACGAGGGGCTG

WI-7233b	213	C T	---	CGATCGTACTGCCAGTAGCATTGCTGTGTCTCCGGTCTTGTTGTACATTCACATTTTCAATTGTTACA GATGTGAACTTTATTCCTTGTCACTAATTATATTTAAATTTATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTAGCCCTCTACTTCTCTTCCACCCTTTTGTGGCAATATTAAAGTGAACCTGCTAATA GTGTAAAGTAC/JGTGCACAAAACCACTGCCAGATAACCAGAGGGGCGCTG
WI-7233	211	T C	---	CGATCGTACTGCCAGTAGCATTGCTGTGTCTCCGGTCTTGTTGTACATTCACATTTTCAATTGTTACA GATGTGAACTTTATTCCTTGTCACTAATTATTTAAATTTATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTAGCCCTCTACTTCTCTTCCACCCTTTTGTGGCAATATTAAAGTGAACCTGCTAATA GTGTAAAGTAC/JCAGCTGCACAAAACCACTGCCAGATAACCAGAGGGGCGCTG
WI-7238	128	T C	---	GCCTCTACAGACAGCTCACCATTTTGTCTGTATCTGTAACACTTTTGTCTTAGTCTTTCTTCTTG TAAATTTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTTGTTT/CJCCGTT CTGTTTAAACAGAAAATAAAGGAGTGAAGCTCTTTCTCATTTCAAAGTTGCTACCAAGTGTAT GCAGTAATTAGAACAAAGAAGAAACATTCAGTAGAACATTTTATTCCTA
WI-7252f	520	T C	---	CCACAGGATCCAGCCAGCGGCGCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCTGGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCCTGAGGCTGCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252e	552	T C	---	CCACAGGATCCAGCCAGCGGCCCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCTGGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCCTGAGGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252d	540	T C	---	CCACAGGATCCAGCCAGCGGCCCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCTGGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCCTGAGGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252c	552	T C	---	CCACAGGATCCAGCCAGCGGCCCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCTGGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCCTGAGGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252b	540	T C	---	CCACAGGATCCAGCCAGCGGCCCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCTGGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCCTGAGGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCCTCCA

WI-7252a	520	T C	---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGCCCCCTCCACTGCGAGCAGCGCGGGACAGAG GCCTGCCCGGGCGCCAGCCCGGCCCTGGGCTGGAGGCTGCCCCCGGCCCTGCTCTCTGGTCCG GACACTCCTAGAGAACGCGCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCGAGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252	T A	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTTT
WI-7265l	231	T A	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265k	121	T G	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265j	174	T A	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265i	227	T C	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265h	80	T A	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265g	170	T G	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT

WI-7265f	231	T A ---	---	AACTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTT/AAGGAGTAAAGATTGGCCT
WI-7265e	227	T C ---	---	AACTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTT/CJCTTAAGGAGTAAAGATTGGCCT
WI-7265d	174	T A ---	---	AACTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGT/ATATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGGCCT
WI-7265c	170	T G ---	---	AACTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGT/ATATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGGCCT
WI-7265b	121	T G ---	---	AACTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGT/ATGTTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGGCCT
WI-7265a	80	T A ---	---	AACTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTTCAGTATGTT/ATATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGGCCT
WI-7281b	183	C ---	---	GATCACCCAGCCACAAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCTCGGGAAGCTTTCTGGCCAAAGTCTGCCAGCCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGCAAAAACGGAGTCCGAGGCCGCGAG GTGTTGTGAAGACCACTCTGTTGTGGTGGGTCTGCAAGAGGCCCTCTC
WI-7281	171	C A ---	---	GATCACCCAGCCACAAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCTCGGGAAGCTTTCTGGCCAAAGTCTGCCAGCCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTC/C/ATTTGGCAAAAACGGAGTCCGAGGCCGCG CAGGTGTTGTGAAGACCACTCTGTTGTGGTGGGTCTGCAAGAGGCCCT



WI-7282b	159	G C ---				TGTCACCTGGCACATTCATTTCTCAGTTGAAGAAGAGAAAAATTTGAAAAATGTCCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTGAAGTGTTCACACTCAAAATATGTCAACTTNNNNNNNNNT AGGCCCTTTTCATAAAAACCAAACTG/CJTAGCAAGATGCAAAATGCATGGCAAAATCTGTGGTCTCCA GTTGGTTATCTGAATAGTGTACCAATTCACCAAGACAGTGTGAGATTGG
WI-7292	92	T C ---				CTTGATTACTTCCACTGAGGTGGGAGCATCTCCAGTCTCCCAATATATCTCCCCACTCCACTAC TCTCTTCTCCACTTTCATTTTCC/CJTTGTCCTTCTCTAATTCAGTGTTTTGGAGGCCCTGACTTG GGGACAAACGTATTATGATATTATGCTGTTTCCCTTCTCCCAATAGAAGATAAGTGCATGGAGCC TGAAGGTCCTAGTTGACTTACTGACAAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A G ---				AACTATGGCAGTGGTCTGGTTATAGTAGAGGGGGTATGGTGGTGGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTG A/GJCGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATTACAGTGGACAAACAGCA ATCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301e	94	T G ---				AACTATGGCAGTGGTCTGGTTATAGTAGAGGGGGTATGGTGGTGGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTG/CJTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATTACAGTGGACAAACAGCAA TCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301d	138	A G ---				AACTATGGCAGTGGTCTGGTTATAGTAGAGGGGGTATGGTGGTGGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGT/A/GJTAACATATGGTGGTGGGAACTATAATGATTTGGAAATTACAGTGGACAAACAGCAA TCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301c	211	A C ---				AACTATGGCAGTGGTCTGGTTATAGTAGAGGGGGTATGGTGGTGGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATTACAGTGGACAAACAGCAATCA AATTATGGAC/A/CJCATGAAAGGGGCGAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301b	182	C T ---				AACTATGGCAGTGGTCTGGTTATAGTAGAGGGGGTATGGTGGTGGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATTACAGTGGACAAACAGCAA TCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301	88	G T ---				AACTATGGCAGTGGTCTGGTTATAGTAGAGGGGGTATGGTGGTGGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTG/CJTTGGGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATTACAGTGGACAAACAGCAA TCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGAAGAAGCTCGGGCAG

WI-7301	205 A C ---	---	---	A A C T A T G G C A G T G G T C T G G T T A T A G T A G T A G A G G C G G T A T G G T G G T G G C A C C A G G A T A T G G A A A C C A A G G T G G T G G A T A T G G T G G C G G T G T G G A G G A T A T A T G G T T A C A T G A A G A G G A G G A A T T T T G A C G G T A G T A A C T A T G G T G G T G G G A A C T A T A T G A T T T T G G A A T T A C A G T T A C A G T G G A C A C A G C A A T C A A A T T A C T G G A C A C A T A A A G G G C A G T T T G G T G G A A G A A G C T C G G G C A G
WI-7314c	49 G A ---	---	---	C T C T C C T T T T T C T C A G A T C T G C T C C T G G T T T A A T T G G G A G G T C A G A T T G T T C T A C C T C A C T G A G A G G G A A C A G A A G G A T A T G C T T C C T T T G C A G C A G T G T A A A A G T C A A T T A A A A C T T C C C A G G A T T C T T T G G A C C C A G G A A C A G C C A T G T G G G T C C T T C T G T G C A C T A T A A C G C T T C T T T C C C A G G A C A G A A A T G T A G T A C C T T A T T T T A T T A A C A A A C T T G T T T T
WI-7314b	49 G A ---	---	---	C T C T C C T T T T T C T C A G A T C T G C T C C T G G T T T A A G T G A C A A A A G G T G G G T G G C A C C A T G G C A T G A G G A A G A G A G G A A C A G A A G G A T A T G C T T C C T T T G C A G C A G T G T A A A A G T C A A T T A A A A C T T C C C A G G A T T C T T T G G A C C C A G G A A C A G C C A T G T G G G T C C T T C T G T G C A C T A T A A C G C T T C T T T C C C A G G A C A G A A A T G T A G T A C C T T A T T T T A T T A A C A A A C T T G T T T T
WI-7314	36 A G ---	---	---	A C T A G G A A G G A T G C C C C A T T A A A G T G A C A A A A G G T G G G T G G C A C C A T G G C A T G A G G A A G A A C A A G G T C C C T G A G C A G G C A C A A G T C C T G A C A G T C A A G G A C T G C T T T G G C A T C C A G G C C T C C A G T C A C C T C A C T G C C A T A C A T T A G A A A T G A G A C A A T C A A A G N N N N N N N N A G G T G G C A C A C C C A T C C T T G T T G C T G G G G T G T G G C A G C C A C A T C C A A G A C T G G A G C A G C A G G C T G G C C A
WI-7321b	199 C T ---	---	---	A C T A G G G A A G G A T G C C C C A T T A A A G T G A C A A A A G G T G G G T G G C A C C A T G G C A T G A G A A G A A C A A G G T C C C T G A G C A G G C A C A A G T C C T G A C A G T C A A G G A C T G C T T T G G C A T C C A G G C C T C C A G T C A C C T C A C T G C C A T A C A T T A G A A A T G A G A C A A T C A A A G N N N N N N N A G G T G G C A C A C C C A T C C T T G T T G C T G G G G T G T G G C A G C C A C A T C C A A G A C T G G A G C A G C A G G C T G G C C A
WI-7321	199 C T ---	---	---	A G A C A T T C T G C T C C C T G A A A G A C T G A A G A A A G T A G T A G T G C A T G G A C C C A C G A A A C T G C C C T G G C T C C A G T G A A A C T T G G G C A C A T G C T C A G G C T A C T A T A G G T C C A A G A G T C T T A T G T T A G C C C T G G C A G G C A G G T T T A T T A A A A T T C T G A A T T T T G G G A T T T C A A A A G A T A A T A T T T A C A T A C A C T G T A T G T T A T A G A A C T T C A T G G A T C A G A T C T G G G C A G C A A C C T A T A A A T C A A C A
WI-7336b	248 A C ---	---	---	C T C T T T C T C A G C A C A T T G A T G G C A A C T A G A A T T A C A G C A G T T T C A A A C T C T A C C A T G G A T A A T G C A A A C A A C C G A A G C T A C A T G C C A A T G A T A G T G C A A A G A A T A T T G C A A A A G G T G C T T A C C T T G A G C C A T T A T T T G T G C A G A G A A C A A A A G A A C A G A A T C A A T A T A A A T T C A A A G A C T A T C T G C A G C T A G T G T G T T C T C T T A C A C A C A G A T A T A T A C A C A G A C A T C A G A A A A T T C T G T T
WI-7338c	221 A G ---	---	---	

WI-7338b	125	A C ---	---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTGCTTTT[A/C]CCTTG AGCCATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTTCTTCTTTACACATATACACAGACATCAGAAAATCTGTT
WI-7338	125	A C ---	---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTGCTTTT[A/C]CCTTG AGCCATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTTCTTCTTTACACATATACACAGACATCAGAAAATCTGTT
WI-7338	221	A G ---	---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTGCTTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTTTCTTCTTTACACAC[A/G]TATACACAGACATCAGAAAATCTGTT
WI-7384c	146	T A ---	---	---	CCATGTCAATGAAATGCTAGGGGGCCAGGGAACAAAATTTTAAAAATAAATAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATACATTGTATTTCATTGTGAACAGGATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTTAAAAAGAA
WI-7384b	146	T A ---	---	---	CCATGTCAATGAAATGCTAGGGGGCCAGGGAACAAAATTTTAAAAATAAATAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATACATTGTATTTCATTGTGAACAGGATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTTAAAAAGAA
WI-7384	145	T A ---	---	---	CCATGTCAATGAAATGCTAGGGGGCCAGGGAACAAAATTTTAAAAATAAATAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATACATTGTATTTCATTGTGAACAGGATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTTAAAAAGAA
WI-7388c	106	A T ---	---	---	TGAAATCCTGGGTCTCTGGCCTGCTGTAGCTGGTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTTATCAAGAGTCTGAAGCGACT[A/J]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTGTGCTGTCTCAAGAACTTTTCCCCCAAGATGIGTATAGTTATGG
WI-7388b	106	A T ---	---	---	TGAAATCCTGGGTCTCTGGCCTGCTGTAGCTGGTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTTATCAAGAGTCTGAAGCGACT[A/J]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTGTGCTGTCTCAAGAACTTTTCCCCCAAGATGIGTATAGTTATGG

WI-7388	94	T A ---	---		TGAAATCCTGGGCTCTTGGCCTGCTGTAGCTGGTTATTTTACTTTGCCCTCCACATTTT TGAGATCCATCCTTTATCAAGAAAGT/AJCTGAAGCGACTATAAAGGTTTTTGAAATTCAGATTTAAAA ACCAACTTATAAGCATTCGAACAAGTTACCTCTATTTTGCCACAAGCGTCTCGGATTGTGTTGA CTTGCTGTCTCCAAAGAACTTTTCCCAAGATGTGTATAGTTATGG
WI-7438	64	A G ---	---		TTAGATTTTAATTGGCAACCAGCAACTCACTGCCACCATCCACTGCAGATCTNCTATTCTCGG[A/G] GTTGATATGACAAGGAAACCTATTGGAACCAAGTCTTCAGATTGTCAGATGTCAGACAGGCTCCT TGCTGTAGGTGTAGTGCATGTACACTGTACTGTTCACCTGTACATAGTTTGTCNCTGGTATTGTTA TTGGAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152	T C ---	---		CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCTGTATGCACTGTCTGAATGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTGTTTAAAGTTATTTAGCCACCACAAAGAGGTTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGCTACTTCTCAAAATGTTTTGACA
WI-7454	152	T C ---	---		CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCTGTATGCACTGTCTGAATGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTGTTTAAAGTTATTTAGCCACCACAAAGAGGTTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGCTACTTCTCAAAATGTTTTGACA
WI-7464c	177	G C ---	---		AATTTGAAAATCTGAAAAAAGTGTCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAATGCACATAAATCTATTATTAATTCCTATGTA CAACAGAGCCACAGCACAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGGAAGCAACGTTCCACCAACAATTAT
WI-7464b	168	C A ---	---		AATTTGAAAATCTGAAAAAAGTGTCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAATGCACATAAATCTATTATTAATTCCTATGTA CAACAGAGCCACAGCACAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGGAAGCAACGTTCCACCAACAATTAT
WI-7464a	103	C A ---	---		AATTTGAAAATCTGAAAAAAGTGTCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAATG[C/A]ACTAAATCTATTATTAATTCCTAT GTACAACAGAGCCACAGCACAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGGAAGCAACGTTCCACCAACAATTAT
WI-7499b	134	T G ---	---		CAATTCCTCAATCCAACTAGTCTGNTGCCTAAACCATCCAGACAAACTCCACTTCGAAGGTTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTCAIT /GJTATAGTCCTTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGCCCTTTTTTAGGA ACTCTGTACAAAATTCCTTTGAAAATATAAATTTTGGAAATGAGTGATGA

WI-7499a	33 A G ---	---	---	CAATTCATCCAAACCTAGTCTGINTGCCTAA/JGJCATTCCAGACAAACTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCAGAGGCACATCAGTTCTTTGAATGCTTC ATTATAGTCCCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGAA CTCTGTACAAAATTCCTTTGAAAATATAAATTTGGAAATGAGTGATGA
WI-7506b	118 A C ---	---	---	TGGGAATAGTAAGAGAAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGTAGTCTGGTGGCTGATTGCCAGC/A/CJGGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAATATTGGACCACTCTTGTTCTACCATCCCTACCCACT
WI-7506	118 A C ---	---	---	TGGGAATAGTAAGAGAAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGTAGTCTGGTGGCTGATTGCCAGC/A/CJGGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAATATTGGACCACTCTTGTTCTACCATCCCTACCCACT
WI-7534b	143 C T ---	---	---	TGTGAATCTTAGCTCTGGAAGGTGTTTATGCCCTTTCGGGGTTCTTGATGTTCGCAGTGTCAACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGGTGGAACACATTCOCGGTATAGAAATGCT AAATTGT/C/JTGTGAAATAGGTAGAAATTTTCTTTAAATATGTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ---	---	---	TGTGAATCTTAGCTCTGGAAGGTGTTTATGCCCTTTCGGGGTTCTTGATGTTCGCAGTGTCAACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGGTGGAACACATTCOCGGTATAGAAATGCT /CJAAATGTCTGAAATAGGTAGAAATTTTCTTTAAATATGTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ---	---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGAGACTTTGAAGACC AGTCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCCTCCTTTGCTCTT/GA/JGGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162 G A ---	---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGAGACTTTGAAGACC AGTCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCCTCCTTTGCTCTT/GA/JGGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60 T C ---	---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTT/CJCTA AAAAGAAAGTGTGATGTTGTGTGATGATCAGCAGCTAAGTCTGCATCTCTGTTAAAGCCACTTGGGTC ATAAGAGGGGAAGTAAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAAGTACATTTAGT ATGGCAATTGAGTTGTGATATAGTTTTCATTTGATGTGCAATTTTGAATTTACAG

WI-7555b	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC/TCTCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCATTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGGGAAGTAAATAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTGAATTCAG
WI-7555	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC/TCTCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCATTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGGGAAGTAAATAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTGAATTCAG
WI-7567b	290	G T ---	---	TGAGCCATCACTAGAAAGAACCCATTTTCAACTGCTTGAACCTTGCCTGGGGTCTGAGCATGAT GGGAATAGGGAGACAGGTAAGAAAGGGCCCTACTCTCAGGGTCTAAAGATCAAGTGGGCTGG ATCGCTAAGCTGGCTGTTTGTGATGCTATTTATGCAAGTTAGGGTCTATGATTTAGGATGCGCTAC TCTTCAGGGTCTAAAGATCAAGTGGGCTTGGATCGCTAAGCTGGCTGTTT
WI-7569b	63	T C ---	---	AATGTATCCCTTTCGGTCCACAACAGGAAACCTGACTGGGCAGTGAAGGAGGGATGGCATTC/C AGCGTTATGTGTAAACAAAGTATCTGTATGACAACCCGGGATCGTTTGCAGTAAGTAACTGAATCCAT TGCGACATTGTGAAGGCTTAAATGAGTTTAGATGGGAAATAGCGTTGTTATCGCCTTGGGTTTAAAT ATTGTAGATTCCACTTGTATCATGCGCTACCCGAGGAGAAGGAGTTTG
WI-7574c	216	A G ---	---	GCCACAGCAGAAATGGAGCGGTGTAGGAAGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTCGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCAGGGC/A/GTCTGCTGGCTGACCAGTTACTCATCCCGTTA
WI-7574b	216	A G ---	---	GCCACAGCAGAAATGGAGCGGTGTAGGAAGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTCGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCAGGGC/A/GTCTGCTGGCTGAACAGTTACTCATCCCGTTA
WI-7574	216	A G ---	---	GCCACAGCAGAAATGGAGCGGTGTAGGAAGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTCGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCAGGGC/A/GTCTGCTGGCTGACCAGTTACTCATCCCGTTA
WI-7576c	168	A T ---	---	AATGATGATGATAATGATGATGACGACGACAACGATGATGCTTGTACAAGAAAACATAAGAGAGC CTTGGTTCATCAGTGTAAAAAATTTTGAAGGCGGTACTAGTTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTAAAACTGGCATCTGACACAAAAAA/A/TGTTGAAGGCCCTTATTCTACATTTACACCTAC TTTGTAGTGAGAGAGACAAGCAAGCAANNNNNNNNNNAAGAAAAAATAAAC

WI-7576b	168	A T ---	---		AATGATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAAACAAGAAAAACAATAAGAGAGCCTTGGTTCATCAGTTAAAAATTTTGAAGGCGGTACTAGTTCAGACACTTTTGGAAAGTTTGTGTCTGTTGTTAAACTGGCATCTGACACAAAAA[A/T]GTGTAAGGCCCTTATTCTACATTTCACTACCTACCTGTTGTAAGTGAGAGACAAGAAGCAANNNNNNNNNNAAGAAAAATAAAC
WI-7577g	77	T C ---	---		AACCATGTTCCCTTCTCTTAGCACCACAATAATCAAAACCCACAATAAGTGTGTTGCTTCCCTTTAA AAATATGCA[T/C]CAAAATCGTCTCTCATTACTTTCTCTGAGGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAAGAGAAAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577p	50	G C ---	---		AACCATGTTCCCTTCTCTTAGCACCACAATAATCAAAACCCACAATAAGTGTGTTGCTTCCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAAGAGAAAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577o	157	G A ---	---		AACCATGTTCCCTTCTCTTAGCACCACAATAATCAAAACCCACAATAAGTGTGTTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGTTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCAATTTGGTTTACAC[G/A]TAGGAAAGAAGAGAAAGCATCAAAGTGGAGATATGTTAACT ATTGTAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577n	48	A G ---	---		AACCATGTTCCCTTCTCTTAGCACCACAATAATCAAAACCCACAATAAGTGTGTTGCTTCCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAAGAGAAAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577m	84	G A ---	---		AACCATGTTCCCTTCTCTTAGCACCACAATAATCAAAACCCACAATAAGTGTGTTGCTTCCCTTTAA AAATATGCATCAAAAT[G/A]TCTCTCATTACTTTCTCTGAGGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAAGAGAAAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577l	93	T C ---	---		AACCATGTTCCCTTCTCTTAGCACCACAATAATCAAAACCCACAATAAGTGTGTTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATT[C/A]CTTCTCTGAGGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAAGAGAAAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577k	154	C A ---	---		AACCATGTTCCCTTCTCTTAGCACCACAATAATCAAAACCCACAATAAGTGTGTTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGTTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCAATTTGGTTT[A/C]A[ACGTAGGAAAGAAGAGAAAGCATCAAAGTGGAGATATGTTAACT ATTGTAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC

WI-7577j	117	A G ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577i	77	T C ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577h	50	G C ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577g	157	G A ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577f	48	A G ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577e	84	G A ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577d	93	T C ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577c	154	C A ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC



WI-7577b	117 A G ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTACTTTCTCTAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTAATTC
WI-7577	107 G A ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTACTTTCTCTAGIG/AIGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTAATTC
WI-7619q	106 C G ---				ACAAGGCGACTTGAAGAGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTC/GJCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCTCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---				ACAAGGCGACTTGAAGAGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---				ACAAGGCGACTTGAAGAGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCTCTCT CGCTTCTTCTTACACAGAAACAT/GJACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---				ACAAGGCGACTTGAAGAGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCTCTCT CGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99 C T ---				ACAAGGCGACTTGAAGAGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG TGGCAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---				ACAAGGCGACTTGAAGAGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCC[G]CTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619j	206 T G ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAAATTAC CAGGAAGATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGC[T/G]TCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619i	106 C G ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619h	150 T C ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAAATTACATGG CAGGAAGATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTC TCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619g	228 A G ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAAATTACATGG CAGGAAGATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619f	237 G C ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAAATTACATGG CAGGAAGATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619e	99 C T ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAAATTACATGG TGGCAGGAAGATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTC TCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619d	189 T A ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAAATTACATGG CAGGAAGATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTC TCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC

WI-7619c	90 C ---	---	ACAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTATCC[C/G]CTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTCTCCCTTTTCCATCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTCTCTCCCTTTTCCATCTTTTCCATCTTTTCCCTCTCT CGCTT/GTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTCTCTCCCTTTTCCATCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAACAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGC[A/G]TTAAACACATCATGGACCAATGTG CCATACTAATGATGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTATAGTAACCAATTTCCCTTGGACTGTTCA
WI-7626c	155 C T ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAACAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACACATCATGGACCAATGTGCCA TACTAATGATGAGCATTTAG[C/T]ACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTATAGTAACCAATTTCCCTTGGACTGTTCA
WI-7626b	28 T A ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAACAAAGCAACAG TAATCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACACATCATGGACCAATGTG CCATACTAATGATGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTATAGTAACCAATTTCCCTTGGACTGTTCA
WI-7626	144 T C ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAACAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACACATCATGGACCAATGTGCCA TACTAATGATGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTATAGTAACCAATTTCCCTTGGACTGTTCA
WI-7689c	134 A G ---	---	TCCCATAAACCGCTGATTCAGGGTCTCTGCTGCCGCCCAACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTGTTCTCTAAAJA /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGGTGGCCACAAATAAATGGATTATTAGAAATTTATATGAC

WI-7689b	134	A G ---				TCCATAACCGCTGATTCAGGGTCTCTGCTGCGGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAAAG /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGGGTGCCACAAATAAAATGGATTATTAGAATTCATATGAC
WI-7689	121	G A ---				TCCATAACCGCTGATTCAGGGTCTCTGCTGCGGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAA AATAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGGGTGCCACAAATAAAATGGATTATTAGAATTCATATGAC
WI-7690	45	G A ---				TGGAGAACATTCATCTTGCCTGCTACTTATCATCAATGAAGATTG/AJCACTGAGATCCAGAGAGG CTGGATGACTTGTCAAGTTCACCGATGGTAGTGGCAAAGAGAGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTCCCAAAAGCTCAGTAGGAGGATGTTCCAGTGGATGAGGGCCACCCAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAACCTGTCAGTTCATCC
WI-7703b	164	T C ---				ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTACATTTGGAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAAGTAAAT/CJGGTCTCTCAGTTGTTTATTTAACCTCTAAATTCT TTCAITTTAGGGGTAGCATTTGTGTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156	T C ---				ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTACATTTGGAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAAGTAAAT/CJAAAGTAAATGGTCTCTCAGTTGTTTATTTAACCTCTAAATTCT TTCAITTTAGGGGTAGCATTTGTGTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---				TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCATTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCCGAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCAGTGGGTCTGGGGCTCGGAGCCTCATCCGAGGAGGTCAGGA GAGGGCAGAACAGCGCTCTGTGTCAGCCAGCAGCAGCAGCTCTCAGCC
WI-7743d	275	C T ---				TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCATTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCCGAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCAGTGGGTCTGGGGCTCGGAGCCTCATCCGAGGAGGTCAGGA GGGCAGAACAGCGCTCTGTGTCAGCCAGCAGCAGCAGCTCTCAGCCAAACG
WI-7743e	106	C A ---				TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCATTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCCGAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCAGTGGGTCTGGGGCTCGGAGCCTCATCCGAGGAGGTCAGGA GAGGGCAGAACAGCGCTCTGTGTCAGCCAGCAGCAGCAGCTCTCAGCC

WI-7743d	275 C T ---	---	---	TTAATGAGTGTGTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGATTCTGCTACCTCACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743e	106 C A ---	---	---	TTAATGAGTGTGTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275 C T ---	---	---	TTAATGAGTGTGTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743c	106 C A ---	---	---	TTAATGAGTGTGTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743b	275 C T ---	---	---	TTAATGAGTGTGTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	106 C A ---	---	---	TTAATGAGTGTGTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743	275 C T ---	---	---	TTAATGAGTGTGTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7758	144 A G ---	---	---	TGACATTTATTCAAAGTTAAAGCAACACTTACAGAAATATGAAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTTCAGAGCTTCAGAGACTTCGTAATTAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATC[A/G]TAGTTTAAAGTGCATTATAATTTTATAACAGAAATTAAGTAGATTTTAAAA GATAAAATGTGTAATTTTGTATTATTTCCCATTTGGAGTGTAACTGACTGCC

WI-7765b	126	GC	---			ACAGGCGCTTGGCAGGTGCAGCCCCCACTGCCCTTGACCTGCCCTTCATGCATGGAAATTCOCCT TCATCTGGAACCATCAGAAACCCCTCACACTGGGACTTGCAGAAAGGGTCAGTATGG(G/C)TTAGG GAAACATTCATCCTTGAGTCAAAAATCTCAATCTCCCTATCTTGGCACCCCTCATGCTGTGTG ACTCAAAACCAATCACTGAACCTTGTGCTGAGCCTGTAATAAAGGICGGA
WI-7773b	237	CG	---			TTAATTTACTGATTCAGCAAGACCAATCATTTGATATCAGATTATTTTAAAGTTTATCCGTAGTTTT GATAAAGATTTTCTATCTTGGTTCTGTCAGAGAACCTATAAGTGTCTACTTTGCCATTAAAGGCA GACTAGGGTTCTATCTTTTACCTTTNNNNNNNTGTAAAGTCTAGTTACCTACTTTTCTTT GATTTTCGACGTTGACTAGCCATCTCAAGCA(G/C)TTTCGACGTTTGA
WI-7774b	170	TC	---			TGCAACCTCTTTTCGTGATGGCAGCTGCTGGTCAGCACTCCAGTAGCGAGAGACGCCACCCAGAAT CAGATCCAGCTTCGGCATTTGATCAGACCAACAGTGTCTTCCGGGGAGGAAACACTTTTTTAA TTACCCCTTTTCGAGGCCACCCCTTAACTGTCTT/CJATACCTTGCTTATTAAATGAGCGACTAAA ATGATTGAAAATAATGCTGTCTCTTGTAGTCAAGTAAATGTGCTTGTCT
WI-7785c	165	G	---			GCAGAGACCTTCCAAAGGACATATTGCAGGATCTGTAAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCATTGGAATAAACTGTCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAAATCAATATTATTATCACAATTACCA TAATTTATTTGTCCATTGATGATTTATTTGTAAATGTATCTTGGTCTGC
WI-7785b	165	G	---			GCAGAGACCTTCCAAAGGACATATTGCAGGATCTGTAAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCATTGGAATAAACTGTCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAAATCAATATTATTATCACAATTACCA TAATTTATTTGTCCATTGATGATTTATTTGTAAATGTATCTTGGTCTGC
WI-7785	156	T	---			GCAGAGACCTTCCAAAGGACATATTGCAGGATCTGTAAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCATTGGAATAAACTGTCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANN- /JNNNNNNNGCCAAAGGCTAAATCAATATTATTATCACAATTACCATAATTTATTTGTCCATTGA TGATTTATTTGTAAATGTATCTTGGTG
WI-7789c	84	GA	---			TCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCAAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA(G/A)TTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAAGTGAAGTCCCTCAGGCCCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7789b	84	GA	---			TCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCAAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA(G/A)TTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAAGTGAAGTCCCTCAGGCCCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT

WI-7789	73 GA ---	---	---	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGACCACATCTTACAGAGACTCTCCC TGACG[G/A]TGGAAATTTAAGTTAGGGTCCCTAAAGCAATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTCAGGCCCGCTGCCCTAGGATAT GCOCTCCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCAGGACCCCATCT
WI-7790b	190 CT ---	---	---	AATTGTCAGTCACTCTTCAAAACCTTACAGTCTTCTCCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTCTTATGTGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAGTTGTGTTCTATTTCTTGAAGTCTC[G/T]TCTATACTTT AAGATACCTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAG
WI-7790	190 CT ---	---	---	AATTGTCAGTCACTCTTCAAAACCTTACAGTCTTCTCCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTCTTATGTGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAGTTGTGTTCTATTTCTTGAAGTCTC[G/T]TCTATACTTT AAGATACCTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAG
WI-7795b	81 CA ---	---	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTCTCAT CTTGATGATGAT[C/A]GTCAATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCCAACATATAAATGTACTTTTCTCCAGAAAAATCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7795	81 CA ---	---	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTCTCAT CTTGATGATGAT[C/A]GTCAATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCCAACATATAAATGTACTTTTCTCCAGAAAAATCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7814c	41 GA ---	---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGATAAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814b	41 GA ---	---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGATAAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814	28 GA ---	---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGATAAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA

WI-7830d	150 C T ---	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/][T]TAAATGTACACATTCGATTTTGATAAAATTAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTTGTCTGCACITTTTACTTTTTTGCCTGTGGA
WI-7830c	54 G A ---	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTTGTCTGCACITTTTACTTTTTTGCCTGTGGA
WI-7830b	134 G A ---	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC G/ATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTTGTCTGCACITTTTACTTTTTTGCCTGTGGA
WI-7830	44 A G ---	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTTGTCTGCACITTTTACTTTTTTGCCTGTGGA
WI-7865e	25 C T ---	---	---	CCACTTCCTATCTGATTTTCCAG[C/][T]AAATGAGGCGAGGCAATTCAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865d	191 C T ---	---	---	CCACTTCCTATCTGATTTTCCAGCAAATGAGGCGAGGCAATTCAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGT[C/][T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865c	25 C T ---	---	---	CCACTTCCTATCTGATTTTCCAGCAAATGAGGCGAGGCAATTCAGTCTTCCACAAACATCTAGCC GCCATCTAAATGGAGAGATGAATCAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865b	191 C T ---	---	---	CCACTTCCTATCTGATTTTCCAGCAAATGAGGCGAGGCAATTCAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGT[C/][T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA



WI-7865	25	C T	---			CCACTTCCTATCTGATTTTCCAG[C]/AAATGAGGCGAGCAATTCTAGTCTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865	191	C T	---			CCACTTCCTATCTGATTTTCCAGCAATGAGGCGAGCAATTCTAGTCTCCACAAAACATCTAGCC ATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGTT ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C]/GAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92	A C	---			TTCAAAACACCTGTCTCCACCCCTCCACCATCTGTGCAATCACTCACCCCTCAGCCTCAGCCTCAGTCCCC CTAACAAATTACCCGTGCAAGAG[C]/GAGTGCAGCTCAGGTGGATTTAATGTGGGTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTTCTTTAAGTAACCATTTCTGTCTTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTGGATTTAAGG
WI-7867b	92	A C	---			TTCAAAACACCTGTCTCCACCCCTCCACCATCTGTGCAATCACTCACCCCTCAGCCTCAGTCCCC CTAACAAATTACCCGTGCAAGAG[C]/GAGTGCAGCTCAGGTGGATTTAATGTGGGTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTTCTTTAAGTAACCATTTCTGTCTTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTGGATTTAAGG
WI-7868c	173	C T	---			TTGATCGATCTTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT CACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCA[C]/TTAGAGGCCAGAAAAATGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868b	173	C T	---			TTGATCGATCTTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT CACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCA[C]/TTAGAGGCCAGAAAAATGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868	66	T C	---			ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCAGCTATTAACTCTCAGTGTAGAGGG GTGGGGTGGCGGGAATCC[C]/JATTTATCAGACTCTGTAATGAATATAAATGTTTACTCAGAGGA GCTGCAAAATTGCCTGCAAAAATGAAATCCCAATGAGCAGCTAGAAATTTTAAACATCATCTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG
WI-7870b	85	T C	---			ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCAGCTATTAACTCTCAGTGTAGAGGG GTGGGGTGGCGGGAATCC[C]/JATTTATCAGACTCTGTAATGAATATAAATGTTTACTCAGAGGA GCTGCAAAATTGCCTGCAAAAATGAAATCCCAATGAGCAGCTAGAAATTTTAAACATCATCTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG

WI-7870	76 C T ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTCTGCAGTGATTAGAAGG GTGGGTGG[C/T]GGGAATCCTATTATCAGACTCTGTAATGAATATAAATGTTTTACTCAGAGGAG CTGCAATTGCTGCAAAAATGAAATCCAATGAGCACTAGAAATATTTAAACATCATTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C -- ---	---	---	TTAGGTCTCATGCCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGCCGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAGGGACATGGGAATGAATTTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGCTTCTCCAGAGCACAAAG
WI-7889b	54 C -- ---	---	---	TTAGGTCTCATGCCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGCCGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAGGGACATGGGAATGAATTTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGCTTCTCCAGAGCACAAAG
WI-7894c	142 A G ---	---	---	AGCCACCCCAATATAACTGTTATCCAGAAGCTGTTATGCTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTATGCTCTATTGTTTGGAATTTATTTGCGTATAC ATTATC[A/G]TATGTAATAATTTGCAATTTTTTATTGAAAATTAATGTTCTTGAGATTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---	---	---	AGCCACCCCAATATAACTGTTATCCAGAAGCTGTTATGCTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTATGCTCTATTGTTTGGAATTTATTTGCGTATAC ATTATC[A/G]TATGTAATAATTTGCAATTTTTTATTGAAAATTAATGTTCTTGAGATTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCAGATTGAAACCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC
WI-7900d	128 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCAGATTGAAACCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCAGATTGAAACCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC



WI-7901	33 C T	---	---	AGACITTAGGTACAAATTGCTCCCTTTTATATATAC/JAGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTATTAACACATGGTAAGAC CCTTTTAAACAAACTCCAGGCCCTGGTTGGGGTGGCTGGTTATTGGGCGAGCGCCGTTGGTGGT CACTCAGTGGCTCTGCATGCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901	271 T G	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAAACAGATT GTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTATTAACACATGGTAAGACCT TTTTAAACAAACTCCAGGCCCTGGTTGGGGTGGCTGGTTATTGGGCGAGCGCCGTTGGTGGTCA TCAGTGGCTCTGCATGCTCTGTCATACAGACAGGTAACCTAGTTCTGIGI
WI-7926c	150 C A	---	---	CATTCCGCATCTGTCACCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGACACT TTGGAGATCAGAAATTCATATTAAGCAAGTGATACAAACACAGTATTTGGGAATGCCTTCATT TACAATGCAATACTTAC/JAATTTTAACTCTTTGTAGGAGAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28 A T	---	---	CATTCCGCATCTGTCACCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGACACT TTGGAGATCAGAAATTCATATTAAGCAAGTGATACAAACACAGTATTTGGGAATGCCTTCATT TACAATGCAATACTTAC/JAATTTTAACTCTTTGTAGGAGAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150 C A	---	---	CATTCCGCATCTGTCACCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGACACT TTGGAGATCAGAAATTCATATTAAGCAAGTGATACAAACACAGTATTTGGGAATGCCTTCATT TACAATGCAATACTTAC/JAATTTTAACTCTTTGTAGGAGAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7947b	203 G T	---	---	AAGAGCCAGCAGGTCAAAAGGCCAACACAAACCATAAGCAGCCAGCCACAAAGGCCAGGTCTGT GCTATCAGAGGTACCTCTTTTACAGTTAGAAACACAGCCAGGCCACAGATCCCATCCCTTTCC TGAGTCATGGCCTCAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTTGAAGCCACA GA/GTJCTCTCCCTGGAGCAGCAGACTATGGGAGCCCGAGTGTGCCACCTG
WI-7947	203 G T	---	---	AAGAGCCAGCAGGTCAAAAGGCCAACACAAACCATAAGCAGCCAGCCACAAAGGCCAGGTCTGT GCTATCAGAGGTACCTCTTTTACAGTTAGAAACACAGCCAGGCCACAGATCCCATCCCTTTCC TGAGTCATGGCCTCAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTTGAAGCCACA GA/GTJCTCTCCCTGGAGCAGCAGACTATGGGAGCCCGAGTGTGCCACCTG
WI-7963b	145 T C	---	---	CATGTGCTGCATGAAGAGCTAAATTTAAAGCAAGTAAGACTAATTTTAAATAAAAATGCC ACAAATTCATTTCTCCTTCAAGTATACAAATGGAGTTATCTCTGCCTAAAAAGTGAAGAAAT TGAGTGAATGAT/CJAAATTTGTAAATTTAGGATAGATCCAAAGTTATTTCCCAACTCTTTGTTCC CCATAAAGTTAGGCATGAGGAGGAGCAGTCAATTAAGGCGAGAGACGGGAA

[illegible]

WI-8021b	57 C T ---	---	---	ACAACTCAGAAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATCTCATCTGGAAA[C/T]GATCCC ACGCTTAGAACCTTACCACAAGGAGTTTTCTTGAGTATTCTCAAAGTCTGGTAGGCATTGGA ACTGGTCTTTACCTTGAGATTCTTTCTTTGCGCTCTTATCAAGTCAGCACACACCTTTTCCAAAG GATTTAGCTTGGGCTTGTTAGGGGTGATTCGAATTCGGTGAATGGCA
WI-8021	57 C T ---	---	---	ACAACTCAGAAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATCTCATCTGGAAA[C/T]GATCCC ACGCTTAGAACCTTACCACAAGGAGTTTTCTTGAGTATTCTCAAAGTCTGGTAGGCATTGGA ACTGGTCTTTACCTTGAGATTCTTTCTTTGCGCTCTTATCAAGTCAGCACACACCTTTTCCAAAG GATTTAGCTTGGGCTTGTTAGGGGTGATTCGAATTCGGTGAATGGCA
WI-8024c	206 A G ---	---	---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCACTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTATCACCACAACACCATTTAGCCGCTCTAGCCTCTAA TTCCC[AG/CT]CTAGAACAGCTGGCCCTGGTCGTCAGTACACAAAGGAAGAGC
WI-8024b	206 A G ---	---	---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCACTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTATCACCACAACACCATTTAGCCGCTCTAGCCTCTAA TTCCC[AG/CT]CTAGAACAGCTGGCCCTGGTCGTCAGTACACAAAGGAAGAGC
WI-8077	167 A G ---	---	---	GAATGAGCCTTCTAGCGCGAGGGACCTGCTGCTGTTGTTGGCCTGCACATGCTTCTATGGAATGC TTTTGGCCAAAGCGGGCACTGAGGACTAAGCTCTGANNNNNNINATCGCCCAAACTCCTTTCT AAGGAGTCTGGGTGTCATGCCCTACAAACC[AG/CT]AAATCTCATCAGATGGATTTTATTTAACGTT GTGATTGTGACTTACTTTCCAACTCTGACTCTGGCATAACAAGGGAAAAA
WI-8118f	114 G C ---	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGT[GT/CT]TTTCTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCAITGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40 A G ---	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGCTAAGGAAGC TATGACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGT[GT/CT]TTTCTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCAITGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118 T G ---	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGT[GT/CT]TTTCTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCAITGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44	CT	---			<p>TCTAGGTTTAAATCAAAAGCAATTTGCANTTTGGATTTTGGAAATGA/C/T/CACCTCCCTTGCTAAGGAAGC  TATGTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTTGTTGTTTCTTAGCCTTGGAAGA  TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT  AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA</p>
WI-8118b	88	TC	---			<p>TCTAGGTTTAAATCAAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT  GTACTTCATGCTGTGGAAACT/C/GGCAAATACAGAATGTAGCTTTGTTGTTTCTTAGCCTTGGAAGA  TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT  AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA</p>
WI-8171d	299	CT	---			<p>TTTTCTCTCTCCGCGGGGACCAGGTACCTTCTGGGGCATACAAATGGCAGCAGGGCCTCGGGAAG  AGGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCTCTTGGCACACA  TTTATGAGGGTTGTCCCTGAAGAGAGAGGGCAGGTGGGGAGAGGTTCCCTGTACTTAAGAGAAGGC  ACCAAGTGGGCAAGAGACACAATGAAGAGGATGATGATAAAACAATCACGGCA</p>
WI-8171c	46	AG	---			<p>TTTTCTCTCTCCGCGGGGACCAGGTACCTTCTGGGGCATACAAATGGCAGCAGGGCCTCGGG  AAGAGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCTCTTGGCAC  ACATTTATGAGGGTTGTCCCTGAAGAGAGGGCAGGTGGGGAGAGGTTCCCTGTACTTAAGAGAA  GGCACCAAGTGGGCAAGAGACACAATGAAGAGGATGATGATAAAACAATCAC</p>
WI-8171a	46	AG	---			<p>TTTTCTCTCTCCGCGGGGACCAGGTACCTTCTGGGGCATACAAATGGCAGCAGGGCCTCGGG  AAGAGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCTCTTGGCAC  ACATTTATGAGGGTTGTCCCTGAAGAGAGGGCAGGTGGGGAGAGGTTCCCTGTACTTAAGAGAA  GGCACCAAGTGGGCAAGAGACACAATGAAGAGGATGATGATAAAACAATCAC</p>
WI-8171b	298	TC	---			<p>TTTTCTCTCTCCGCGGGGACCAGGTACCTTCTGGGGCATACAAATGGCAGCAGGGCCTCGGGAAG  AGGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCTCTTGGCACACA  TTTATGAGGGTTGTCCCTGAAGAGAGGGCAGGTGGGGAGAGGTTCCCTGTACTTAAGAGAAGGC  ACCAGTGGGCAAGAGACACAATGAAGAGGATGATGATAAAACAATCACGGCA</p>
WI-8314b	85	GC	---			<p>GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTTGGGTCTGT  TTCTCTATCTCTAAGGG/G/CJAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT  GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCCAATAGAATTC  TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT</p>
WI-8314	78	CG	---			<p>GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTTGGGTCTGT  TTCTCTATCTC/GJTAAGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT  GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCCAATAGAATTC  TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT</p>

WI-8321	178	G A ---			TTTTAAATATGCCCCGTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGTTACTTTTCAAGAGCTGCTGTTATCTACTGAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAAGATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTTGGC
WI-8321	178	G A ---			TTTTAAATATGCCCCGTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGTTACTTTTCAAGAGCTGCTGTTATCTACTGAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAAGATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTTGGC
WI-8321	178	G A ---			TATGACTCACTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTTCCCTTCCCTGTGCAGCCTTAGA/CJACTAAGTAG CAGTACTGTTGGTGTGTTGTTGTTCTTCCCGAGCAATGCCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332b	123	A C ---			TATGACTCACTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTTCCCTTCCCTGTGCAGCCTTAGA/CJACTAAGTAG CAGTACTGTTGGTGTGTTGTTGTTCTTCCCGAGCAATGCCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C ---			TGCGGGCTTAACAGGAAGCATGACTGGGAGGCTCAGGAAGCTTATAATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTCAGATGGCAGCAGGAGGAGAAAGAGAGGAGGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTCCATCGGGAGACAGCAGTGGGGATGGCAGTAAACCATTAGA AACTGCCCCCATGATCCCAATCACCTNTCACAGGCCCTCTCTCCAACACAGTGGGG
WI-8378b	311	T C ---			TGCGGGCTTAACAGGAAGCATGACTGGGAGGCTCAGGAAGCTTATAATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTCAGATGGCAGCAGGAGGAGAAAGAGAGGAGGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTCCATCGGGAGACAGCAGTGGGGATGGCAGTAAACCATTAGA AACTGCCCCCATGATCCCAATCACCTNTCACAGGCCCTCTCTCCAACACAGTGGGG
WI-8378	308	T C ---			TTTAGCACATATTTAGCATTAAGCCTCAACAGTACAGCAATATGTTACATTTCTTGTGAAACAG TTGTTGTAGACTGTTAANNININININAAATGTAACCTCGACTTGGCCTAATAGGATTTGACCNNTAA GAGGNTCTTTGCTGTGGANGGGTGGCTTGTGCTGAACCTCCATCTGTG/GJGCTTGTAGCTGGTG AGGCTGGGAGTATGGANGNCCCGGGGGCTTGGCNATGNATTCAGTGAG
WI-8426	184	T G ---			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTC/AJCA TCTTCTCTATCTAGTCCAAAGTTTGTAGTTTCAATCCCAATTAACCAATCCATGTTATTTAAGA AAAAACCTTCCCAGTTATTGTCAAGAACTATGATTTAGCTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450h	61	C A ---			



WI-8450g	55 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCCAT CTTCTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450f	108 T A ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTCJTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450e	125 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTCJTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450d	125 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTCJTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450c	108 T A ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450b	61 C A ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT TCTTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450a	55 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCCAT CTTCTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8458b	60 A G ---				CAAGGAAAGCTGTCAGTCTTCATAAACTTTCAAAGAGTTTACAAAATACGATTTTTTAAJ/GJCTA CAATTCAGGATTAGCATCCAAACCTACAAACATGATGATACATTCGTACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATACCTTGTAAGAACTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T ---	---	---	CTTCTCTCCAAAATCTACATGAATACITTTGAAGACAATAAATACTACAACCTTACAAATGCCAATTA GACAAAAGAGANTAAATGATATAATAATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTCACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAACATACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---	---	---	CTTCTCTCCAAAATCTACATGAATACITTTGAAGACAATAAATACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATAATCATTTTTTNNNNNNNNCCCTTGCTTATTCACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAACATACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---	---	---	CTTCTCTCCAAAATCTACATGAATACITTTGAAGACAATAAATACTACAACCTTACAAATGCCAATTA GACAAAAGAGANTAAATGATATAATAATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTCACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAACATACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---	---	---	CTTCTCTCCAAAATCTACATGAATACITTTGAAGACAATAAATACTACAACCTTACAAATGCCAATTA GACAAAAGAGANTAAATGATATAATAATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTCACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAACATACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---	---	---	AATAACATGTTATGAACAAGCTGTTACAAGTAGTAGGTAGTACCTTAATTTTGATAAAAAAAT TAAAAAGCAT[A/G]AACATGCATATAAAATAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATATCTCCCTTTGTTTGTCTTTTAAAAAACATTATTTCTGAAAAAATAA ATCAGAAAAACATGATCGTGGAGAGATTATTA
WI-9439b	101 C T ---	---	---	ACAGAAATGACCTTTATTTGTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAATCCAGTCTGTACGTCAGTACCTGT[C/T]GTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACTTAGAAAACAGCCCTACCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTCATAGTTGTCTGAGCTAGAAAACCTGTACCTGTAAACAAAG
WI-9439a	76 C T ---	---	---	ACAGAAATGACCTTTATTTGTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAT[C/T]CCAGTCTGTACGTCAGTACCTGTCTGTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACTTAGAAAACAGCCCTACCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTCATAGTTGTCTGAGCTAGAAAACCTGTACCTGTAAACAAAG
WI-9446b	75 T C ---	---	---	GAAGGCTTGATTAAAGGGAGGNTTTATTTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAAAT[C/C]CTCTAAAGNGACACATGCCCCAAATGACCAANGNCATTAAGCAAAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTTGTGNCCTTACTNTTATCACTGTGCTTCTGCTTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT

WI-9446	75	T C ---	---	GAAGGCTTGATTAAAGGAGGNTTATTGTGATGTNAACCTACCATCCATAGACTATAAAGANCATTA TAAAAAA[T/C]CTCTAAAGNGACACATGCCCAAATGACCANGNCATAGCAAAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTGTGNCCTTACCTATCTACTGTGCTCTCTGCTCTTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185	A --- ---	---	ATTAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACATTTT GAGATAATTATCTAGATTCAGGCTTCTCTAGATGTAGTNCCTAAAGCTTATAGTTTACATTTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTNCTTTAATTAATCAAAAGTATGTTAATGTCACCTT GGAATCTACATGGAAGGCCAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9497	185	A --- ---	---	ATTAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACATTTT GAGATAATTATCTAGATTCAGGCTTCTCTAGATGTAGTNCCTAAAGCTTATAGTTTACATTTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTNCTTTAATTAATCAAAAGTATGTTAATGTCACCTT GGAATCTACATGGAAGGCCAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9523b	193	C A ---	---	GTGAAAAAGTTTCTATTCATTCATCATACATAGATTGTGCTAAGGATCATTTTGGGAAGAATGTG CAGCATTCAGAAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCACA GACTCAGACAATTACAAACTATTTAGCCATGATCTATGGTGAATTTCCACACATTTGTA[C/A]AGTG AAAGCTCTCAGCTTGGAAACAACCTTGCAAGGCAGACTGCATGCACATATAT
WI-9523a	47	G A ---	---	GTGAAAAAGTTTCTATTCATTCATCATACATAGATTGTGCTAAGGATCATTTTGGGAAGAAT GTGCAGCATTCAGAAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCA CAGACTCAGACAATTACAAACTATTTAGCCATGATCTATGGTGAATTTCCACACATTTGTACAGTGA AAGCTCTCAGCTTGGAAACAACCTTGCAAGGCAGACTGCATGCACATATAT
WI-9554	202	T C ---	---	AAAAACACAAGTTTCATACATCACAAAAAACCTTCCATTATAACACAGAAGTGATTATACCAGAC AAGCATCAGTGATGTATAGTCCCTTNCCTAGTTGTTATTGTACAATGCTGTAGATAATGCAGCCCATG CAATACACCCCAAGAACACTAGAGTCTCTACACCAAGTACAATATGATAAAGCAGCCCTCTGCAAGTG GT[C/G]CTGGATACCCACTAAGAAAGTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97	G A ---	---	CCAAAAGCCAAACCATTCATATGATGGATTTCATAAACAATTTATGATCCCTTTTGGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC[G/A]CTTGAAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAATACAGGTAAGTATTCAG GGNTAAATGGTACAAAAAAGGCTGTAACTCTTTNCTTCACATTGATCACA
WI-9625b	172	A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCCTCGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCTCTGGGAAAAAATTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTCT[AT/G]TTTACCAATTTTATATTGACATAA AGTAGCAGACACTAGTTATTTCAATTTAAAAAACAACACTGACAAATCTTTTC

WI-9625	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAACITTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGTTGTGGACAAGTTACTTCTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTTAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	TTTTCTGAGATCAAGAGCTACATTTTGGTTAGTGATGTCTACTATACCTTTTTCATCCTTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTGTAAACAGTGATTCGTAGACCTAAAAATCCAAGCT TACAACTC/TGTGCTTTACCTGATACATTTATCCATTTACTTTCAATTTGGATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGTCCTGCTTTTGTAGTTAATGTGTTT
WI-9676n	114 A G ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCA/G/GATGTGGCTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTTGTTT
WI-9676m	184 G T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTTGTTT
WI-9676l	84 A C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG C/TTCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTTGTTT
WI-9676k	202 C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTTGTTT
WI-9676j	92 C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTTGTTT
WI-9676i	173 T C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTTGTTT

WI-9676h	134	C A	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG C/AJTTCACCTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGC/GTCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG ATTTCACTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGC/GTCATGAAATAACTTGAGG C/TJAGGGTCTCTCAGCTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG ATTTCACTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGC/GTCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG ATTTCACTCAAGGCATCTCAGCAACCCACATGGCTT/CJCCCTCTGTGGC/GTCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG C/AJTTCACCTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGC/GTCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG CCCATTTACCTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGC/GTCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG CCCATTTACCTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGC/GTCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG CCCATTTACCTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGC/GTCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9738b	40 C A ---				TGGACCAACACAGACAGATGATTCCTGGTGGCTGTGTA/C/AJATTACAACCTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTGTGCACCTGGCTGGAGCGGGTGTGTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGGCACATGCTGTATTGCTGTC
WI-9738	40 C A ---				TGGACCAACACAGACAGATGATTCCTGGTGGCTGTGTA/C/AJATTACAACCTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTGTGCACCTGGCTGGAGCGGGTGTGTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGGCACATGCTGTATTGCTGTC
WI-9756	47 A ---				ACTGAAATGTAAATGGCCAAAGCCAGCCAGGACCTTAAAAATCATAAGAGTTAATCTGTGGGAAA GAGTAACATAACAAAGCATCTAAACAAGAGCAGGATGTGTAATGTGTCCTTATCACTTTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTCCACAACACAGAAATATACACTTTTGGAAAG ATTCCACTTAACCACTTGATTCCTCACTTTTATGATTTAAACCTCCGTGG
WI-9758	135 A G ---				GATGGTCCCTTAAGGATTTGCATTGTTAATGGGCAGACTGGTGCAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATTCAAAGAAATCTTGTTCGCAAGGTCAATTTTATACTATTTA A/A/GTAAATAACTCTGGTAGGTTCTATAGCAATGCTAAGTAAAGTAACCGCTGTTTCTAAAT ATTACG
WI-9778	127 G A ---				ATTTAAATCCAGGCAGCGGGGAAATGGATACCTTCATATGTCTGTACCCAACTATAAATTTTG GTTCTCATGCACCATTTTCAATTTGCTTCTCACTCCAAAGTACCAGTATTTACCAATT[G/A]CTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTGCCTCA AAGAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A ---				TCTCCCTTTGCCTCCTCATGCCACTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAATGCAGTTT[C/A]TGGATCCACCCAGGA CTCAAAAAAAGTGGAAATGGGAGAGAGGACCTGGAATCGGTGTTGCTAGCAAGCCGCCAGGTGG TTTGTAAAGTGGACTAAAGTTTGAGGACCAGACATGGAAGGTTGGCTTTGGC
WI-9841	101 A G ---				TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCATTTTGAATGAATAAATATACI/A/GTGTGTATGATATATATATATTAACACTT AGGATTATATACACACAATAAAGCTGTGTAGGATAAATAAGGTTCTATCAGTGGGAAATGAGA TTGAAAGAGGGGATGTGTTACTTGTATGCTGTTG
WI-9880c	222 G A ---				GAACATAACACCTTTCTGCATGGATTTTCTTGATTTATGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTAAAAATTATTTTATATAAGCACATGAA AATGGAATGAAATAATGA/G/ATTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C A ---	---	GAACAAACACCTTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGTCTCTGTGGGGTGGATTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGA/C/A/TATATAAGATCCTCTTTTAAATTTATATTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T ---	---	GAACAAACACCTTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGTCTCTGTGGGGTGGATTTTATGATATCTCTGTAGACCCATAAGGGAGGCTG TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATTTATATTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T ---	---	ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTATTTTAAAAACAACGCCCCAGTTATCACAGTTCTNTTTTGT[C/T]CACC ATTTCCATAACAAAGAAGCTACACAAAATTTGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGTGCATGAATAATGATTCCAAA
FB25G10b	109	A G ---	---	TCCTCAATGACAGATGAACATAATTTCTCTTGGTAAGAAATACITTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAA/A/GTGAATTTAGATCCTCCCCCAG TGACAAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCCTATTTGGATATCC CGGAC
FB25G10	109	A G ---	---	TCCTCAATGACAGATGAACATAATTTCTCTTGGTAAGAAATACITTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAA/A/GTGAATTTAGATCCTCCCCCAG TGACAAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCCTATTTGGATATCC CGGAC
IB3071	102	C A ---	---	ACAACGCTGAACCTCCATAACAGTCAATGGTACAGTCAACATCACATGTACAGAACACACAATTTA GATGAACCTGAAATTTAAGNTAAATAAAATAAAAT[C/A]CAATTTCAAGNAAACAAAAATCAAAAC ATTAAGGNTCCCTGNNATATTTCTAAACCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCAACAATATGACCCCTATTACCCAGTCTAGGGATTCTG
NIB551	161	C T ---	---	CGTCTTTCTTTTGGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATTTGGGTGTCCC TACTGAGCTTGGGGCCAGGTGTGACTTAGAACCCCAATCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGT[C/T]TGACCACATACATGCGGCCATTGGTTGATTTACGCTTT GCAAGCAGCGTAGTGAGAAACCAAAAGCTTGTC
S72904	51	G T ---	---	AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGAAGTCTCTT[G/T]AATTTGTCAGTTC ATTCTGGAAATCTTTTGAAGTAAATAAGGATCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTGCTCAAAACCACAAAGTGTGTAAGTCTCTCCCTTTCTGTCAATTTGGTGTCTTTAAATA TTGCAAAAGTCTGATGCTAAACAGATTTTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	TATCTTTTATCCTGGGCCACAGTCTTGATTATCCTCTTGTTAAAGACTGAATTTGTAAACC CATTCAGATAAATGGCAGTACTTTAGGACACACAAACACAGAGC/TACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGAGCATTTAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTACGCCTCTCTACCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTCTGTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCTTACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACTTCTCACANGCTGTATTACCTTTTACAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGCGAGTGCACAGTGAOC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTCTTTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCTATCACAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAATAAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTGGAAGTGG
ESTC129	20	---	---	---	AGTCACCATGCCAGCCTAGNATGAGTTAGTAAGATTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG



ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCCCTTAGCAAACNCTATGTTGTCTCAGGTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTTGGCTTCTGTCCTCANAGTCTCTCTCCATGTGGCAAACA
ESTC139	45	---	---	---	AGGAGCACAGCCTAAGGACATGAAGGTCAGAGTTTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTTGGTTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCATGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATACTATTTTATTCATTTTAAATC AAAGANACCATTCCTTAACAACA
ESTC143	29	---	---	---	GTTTACGAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCTCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTTCTTGACATGAGGTGCTTTTATAGCAGCATTTCCGG
ESTC146	20	---	---	---	CATGTCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	TCCTTGGTTGCTACACAGACACTTAAGTACTGTATCGCTGTNATGCAGCGGCTGTGGAGGCCCTG GGGGTGGCTGGGCTGTGCTGAG
ESTC149	28	---	---	---	TCAGTTCAATTTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATAATCAATATT AAACCTGATGTTTAAAGAACCCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCAATTTTTTCTTTTAAATACAAATCTACTGGTGTCTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACATACAGTNTTGCAGGAATTATAAGTGGATCAACAATT ATATTATTGATACAACTCATGAGCAATTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGCGCAAAACAAANCCCTGGCTGCCCTCGGGATGGAGCGGGGGGCGCTCA CCACCACCTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTCTGAGGCACATCAGTACGTTGGTCAATTTAGGGCAGGCTCTGGTTCTGCA GCTTGAAGG

ESTC16	23	---	---	---	---	CACTGAATGCTCTGCCATGAGCCNAGCAGCACAGTGATCATCCCCACAAGGACAGGTT
ESTC160	38	---	---	---	---	TTCTAGCATTGCTGGTGAGTGGGGGCTGAGCTGGGNGCAGTCGGCAGTGCTCACTGGGCGCGTTTG GGACTGGGTGA
ESTC162	36	---	---	---	---	CTCTTCGTCGGTTTGCAGTTGCTGTTTGTTCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	---	TCATTCTCCATAGAATATTGGTTTTGTAACANCGAATACAATCCAAATATATAACATTTAAACAATCC GATACATACCA
ESTC169	22	---	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTTGCTGGATTAGAGGAAAGGTGCCCGTCTGTTCCTCATGACTT
ESTC176	23	---	---	---	---	CACCTCCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTCAAAATTTTNCITTTATCTATTAAATACCTTTTAT TCTCTTTATTCCTCATAAAAGGCAACCAA
ESTC18	29	---	---	---	---	TCAGACACTGCCGACATCAGCATTGTCTCNTGTACAGCTCCCTCCCTGCAGGGCGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	---	TAGGGATTCCAAAGTTGCCTGGNTTAAATATAATACATAITTCACAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	---	GCTTGACTAGGGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAATTTGTCATTCAGCTTG ATTTTTCACCTCA
ESTC187	24	---	---	---	---	ACCATGATTGCTCACCACAAAGCAINATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG TCTATTAAACAGGGTTATGTCACACCNCTGTCAACCTCAAAACAGATGATCACTCATCTTGCTCTCCAT CTTGC
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	---	TCCTCAAATACCACCTTTCCCTTAACCTTATCAGTCTAGTAGAGCNTTTCAAAGGAGGAAAATGGGTTAC CTTTCAGGGG
ESTC197	26	---	---	---	---	ATCTCCAGTGTCTGCTGCCCTCTCCNCGCAAAGTCTCCACAAGCACA
ESTC20	33	---	---	---	---	AAGATTAGGACAGACCGGTATAGTAAGCTCTGNGGAACTCCAAAGATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	---	TTTGGTGAAATCCCAATATATGAGTTTTAAAAAATAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGCTGCAACAG

ESTC201	35	---	---	---	---	TCCTACTTGGGTAGTTAGCAACATTTTAAANCCACATCCACAGATTGGTT
ESTC202	22	---	---	---	---	CTGCTGGAGGGAGACAGCGNCGCGCTGGGTGGCGCCGCCAGAAAGGCTGGCGTGATGTT
ESTC203	27	---	---	---	---	CGAGATGAGCC
ESTC208	43	---	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAATTTACTGCAACTTTTGTAGAAATTTTATTGTGCTAC
ESTC210	29	---	---	---	---	AAGACACGTTGCA
ESTC212	27	---	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAACTCTGAGAGGGATAANAGCAATACTATTGTTTAAAGC
ESTC214	21	---	---	---	---	CTAAGAGTGAAAA
ESTC216	49	---	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAGTGAGTGACGGTGACCTGTG
ESTC217	28	---	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGGCTTCAGAGCAGAGGGCTTGGT
ESTC219	32	---	---	---	---	TCAAGTC
ESTC22	41	---	---	---	---	CTCCAGAGTCCCTCCTCANACCAGGGGCGAGGGAGTTAGGGAAT
ESTC223	27	---	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTAATTAATCACAGGTATTNTTAGATTGGTCAGAAAA
ESTC224	37	---	---	---	---	CAAAAGACCA
ESTC225	20	---	---	---	---	TTTTGTCAATGAGCAATACACTGANTGGAATCTGCATGATTAATAACATTAAACAAGTTCAT
ESTC23	27	---	---	---	---	AAACACACCCCA
ESTC230	43	---	---	---	---	GTACACATCCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG
ESTC231	24	---	---	---	---	GCAAAGGAAGC
						TCATTGAAGAAAAATTATGGGTTTTATTCTTATTCTAATTGNGAGAATGCTTAATGTACAGGCTACA
						TAAGGGCC
						CTTCTGAAGCCCAAGAGAGGGGCGAGAANGTAGTCTTGATTTAAAAAACAGAAAGGGGAGGAGGA
						CGAAGGTAGATTCCCTCACATATTACAAAATACACANAACACACACACACACACACACA
						TGCACGTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAAGGA
						ATGTGTAGGATCG
						TTCTACTTTATTTCATATTCCACCACNATAACGACTCCTTTAATTTAACTAAAAACCATACAGGGT
						TCCTGAAAGGG
						GGTTCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
						CAAAAGGGTGTAGTCATATTCCCCANCAACAGCATGATAAAATAATTCAAC

ESTC28	23	---	---	---	---	GAAGAGCTGGGCACGCATCTGACNITTTCTTCTCTATTCTCTATAAAAAATAAAGGAAGCAGAAATCT GC
ESTC3	20	---	---	---	---	CAGACATGACCTACCGTCCCGCCCTCAATTCATATTTTCTTGAGCCGCTTGGTCAGGTTTGAT TCGCACACTCC
ESTC31	32	---	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATAATNTCAGTCGGTGATCATTTGTAATATACAATACAAAG CAATTTCTCAGA
ESTC33	25	---	---	---	---	AGCACTTCCAGCTCTTGACGTTGTGGACCCAGGAACTTCCGGAA
ESTC39	26	---	---	---	---	AAGGAAGGGAACCCACCTGGGCTTTNGGTACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	---	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAATCATTATGCTGATGGAAGAAACCAATT
ESTC40	22	---	---	---	---	GGCATGCTAGACAGAGGCATTANTTTTGAAGATCTTTTAAAAATATTTTGACTTGTTCCTCCCTTCAC
ESTC45	37	---	---	---	---	TTTGGAGGTTTGTGCTGGAGTTTGTCTTTGTAAACNCTCTCATCTCAGGCTATATATTA CTGTCGCTGGTGAGCCCTGCCGCTGTCCCATGGGCCAGGAGCCACTGGTGGGANCCGGGCAGATG TTTACCCCTGT
ESTC50	56	---	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTGGCAGGAAGNAGTGGAGGGAAGGACACCA AGT
ESTC56	45	---	---	---	---	AGTGGCCCTCCCAGTCCCNCTCTGGGCACAGATCCCACAGTCTGCTC
ESTC57	20	---	---	---	---	GAAACACAAAAAGTGTGAGAAAAAACTTCTCAAAATNGTTCAGACTTCAGGAAAAATGATTTCC ACATGGTAAGGCC
ESTC59	38	---	---	---	---	TCTGCAGCACTTCACTACCAAAATGAGCNITTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATG TGGACTGAACCG
ESTC6	27	---	---	---	---	AGTGATTTGGTAGCGGTGTTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC61	57	---	---	---	---	ACAGACACAGCATCACACCANAGGCCACCGGAGGTGCGGGAGACGACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC63	20	---	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCCTCAAGTTTAAATCCACACTTACTTACTGCTCATCCGT CACTTTCGCTAA
ESTC69	20	---	---	---	---	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCTCTGAGTTGCANGCACGATGGAGATTTGGACACT G
ESTC7	45	---	---	---	---	

ESTC72	37	---	---	---	GGGCTTCCAAATGGGTATTGGGGCCAGGAGGCTGGCNTTTGGCGTGACGCCCTAAAAAGTGTGAACC AACAAATTCACAGCTACAGGAAATCTAGAACAATAAATCAAAATATTCATCATCNTTTGGGTTGAAAAGTTG GAAGA
ESTC74	49	---	---	---	ATGACTTTCTGTCCCATCGGAACACAGAGTTTTCCACAGNGAGCCCTTCCTATCTCGGGTTA
ESTC77	40	---	---	---	GGTCTAGCACAGGGATAAGANCCCCACTCGCATGTCCCAGAGGGGCAGCACTCCAG TTTCAGATGATGGGGTCTGAGATGNTCCCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC81	20	---	---	---	CAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC TTTCACAAACCT
ESTC82	25	---	---	---	TTTAGCTGCTATACCAAGTTTCCATAAANCCTGCTGCTGGTGGGGAGGCTACAGCCTGACCACATTC TTTGC
ESTC83	53	---	---	---	ATTGCAAAGGAAGTGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC85	28	---	---	---	CTGGTTCCTCGCTTGGCATTGGCTCCTCCTCNGGCCAGTGTCTCCACCAAGTGTCTTCCCCGATGAT
ESTC89	22	---	---	---	CTCCCCCTCTCAGTTCACAGTGGAGACTANGGAGATTGAGGGCAGGATCC
ESTC90	33	---	---	---	GCACGTCTTTGTTCTCCTCTCCAGAAAGTTGNAGACGCTATTAGTTTGATTATCTGTCG
ESTC93	29	---	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCTTAATTCA GTGGATCTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTTGGCTGTTCTCCA/C/TGCCAG ATCTTATCAATGATCTTTCACCTAAGAAACAGCAAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATGCGATTTTTCACAAAATCAAAGAAGAAAGGCTTAGCTG
DWU-100	127	C T	---	---	TTCCATCTAGATATCTACTCAAATAATTGAGACAAGTGTCAAACAGAAAGACGCTTGTGCTGAA TGTTCAATGGC/GJGCCCTATTACAGTAGCCAAACGATGAAAACACCCCAAGCTATATATTACCA GATGAAAGGATAAACAATAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTATCCCTACTACACTGTGGAT
DWU-177	77	A G	---	---	CAAATACCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATTCAGGGTTAATCCATCTAAGTGAC ATTTTGAATTCACGGGTGCCACCCCAATCATGCCAGCTTCTGTCAATGAATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGGI/CTGGGAACCCAGCCCTATCTGAGTCTTCGGCTCCCTCC
DWU-286	213	A C	---	---	



EST10398 2a	147 C T ---			TGCCTGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGCGCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTTACATTTGGGGCTTGACTTTCCAACACGGAGAAG CAITGTTTCTTCTGTTGGCCAAGAGGTATCTACCAATAGTCTATTAGGCATTTG
ESTD-C7	14 G C ---			ATATCGTGGCCTTA[G/C]TTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C ---			CTTTCATGCACGATAGGCTTTCTCTACTAATACAGAAATTTTGAAGAAGAGCAAAACAACCTTTCAAGG ATAATGGGGCAATCACTTCTTTT[C/T]CTTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A ---			AGTCTCATCTGCGGTGTCAGGTAGATCCCTTTTACCC[G/AJCCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G ---			CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGACGGCGCGCCAGGCTCACTCTATAGTGGGTGCG TATTCGTCCACAA[A/G]TGCATCTGGATCAGCT
ESTD- HRASa	37 C T ---			CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGACGG[C/T]GGCGCCAGGCTCACCTCTATAGTGGGG TCGTATTGTCACAAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G ---			GGAGCAGGAGGTGGGAGGGGTCTGTCTGCTCCAGGTCCACAGACCCAGAGAGCGGCTCAGTG TATCCCCACCCCCA[A/G]TGGGGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18 A G ---			GTGACCTTCTCACTTTAA[G/A]AACCTTACCAGGAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAAATTTAGGATAAACAGAAAGGAGGATGTAAACA
EST36751 7	36 C T ---			CCAAAGTGTTCATTTAGCTTTGCAGGTTTAACT[C/T]GATTACTTTTCTTATTCAAATCTCTGTA AAATTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	109 A G ---			CACGTGGAAGGAGCTATTTTGGAGGCTTAAAGAGTAAAGAATCTGTCCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCATTAAACAAAT[A/G]TTTACCTTTTGAAAAATAA ATGAAGGATTGACCTGCTTGGCTCTGGAAGAGATCCGTACCGTCTGACGTTTTGAAACAATACA GATGCTTCCCTTGTAGCAGTTTTCAGCCTCCTCTACCTA
EST18288 3	121 C T ---			GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGAGGCTGTGACAGGATGGAAGACTGGCTGCCCTGA[C/T]GGGAGCCAGT GTGGACAGCACCCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAGGCAACCTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31 C T ---			GGGAGTGACAGCTAGAGCACCAAGGGGGGCT[C/T]TACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATCTGG
ESTD-ALB	180 A G ---			AATCCCAGCACCTTTAGGAGGCTGAGGCAGGCATATCACAGAGGTGAGGATTTGAGACCAGTCTGA CCAAACATGGTGAACCCCATCTCTACTATAAAATACAAATTAAGCCAGGATGGTGGTGCATGCCTGT AATCCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGAGGCG[G/A]GAGTTGTGGTGAGCCGA GATGGCACCAATTGCACTCCAGCTGGGCAACAAGAGTAAACTCTGTCTTC

EST70523 3	182 G T ---	---	TTCCGCCAGCCCCCATCTTGACACCTGGTCCCTCAGGGGCCACCCCGCGGCACTCACCGCTCT CGCTCTGGTAACATCCGGCCGGCGCCGCTCTTGAACACATAGCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGCCCTTCTCTGTCGGCCCTTGCCAGGGGCCAGCCCT[G/T]CAGAGAGGGGTCCCTGT GGTTGAGCTGAACACACAGCTGTGGAGTGTCTCCACGTG
ESTD- APOA2	101 C T ---	---	CCAGGTGTTGTGGCAGCTGCCTGTAATCCAGCTACTCGGGGAGACTGAGGCATGAGAATCTTTGAAC CGGGAGGGCGGAGGTTGCAGTGAGCTGACATCG[C/T]GCCACTGCCTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ---	---	CAGTGTATCTGAAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGTTACAGGAGGCTTT AAGTTACGACATCTTTGGCTCAGATGAAGGCCAAATCCGAGAGAC[C/T]CTAGAAGATACACGAGAC CGAATGTATCAATGGACATTGACGAGGAACCTTCAACGATACCTGTCTGGTAGGCCAGGTTTATA GCACACTTGTCACTACATTCTGATTGGTGACTCTTGCTGCTAAGAACCTT
EST74167 6	137 C -- ---	---	AGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGGAGCTGCAGGGCGCGCAGCCCGGCTGGGGCGGACATGGAGGA CGTGGGGCGCCCTGGTGCAGTACCGGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGGAGGAGC TGCGGGTGGCCCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTC
EST43211 8	132 C -- ---	---	CGCTGGTGCAGTACCGGGCGAGGTGCAGGCCATGCTCGGCCAGACACCGAGGAGCTGGGGTGCG CCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATCCGATGACCTGCAGAACGCC TGGCAGTGTACAGGCCGGGGCCCGAGGGCGCGGCGGCTCAGCGCCATCCCGGAGCGGCTG GGCCCTCTGGTGAACAGGGCGCGTCCGGCGCCGCACTGTGGGCTC
ESTD- ARSB	126 A -- ---	---	GGAAGAAATGGAGCCTGTGGGAAGGAGCGCTCGAGGGTGGCTTGTGGCAAGCCCTTGCTGA AGCAGAAAGGGGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAACCATCATGTGAA GGAAGCCCATCCCCCAGAATTGAGCTGCTGCATAATATTGACCCAAAC
EST36770 4	144 C -- ---	---	TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGGCAGCTATAATCC ATCGAAATGTATTTTCATTGAGAACACCAATATTACAGTTGTGCTTTCCATTATGATCCCCAAAT TCAACCCCTCCGATAGGGCTGGCCCTGACCAAAATATACTGGGTTTCCCTTTCTTCTGATCAT TCTTACAAGTTACTCTTATTGGAAGGCCCTAAAGAAGGCTTATG
EST26021 1	137 A -- ---	---	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTGAGGTTGAGTGACATGTTCCGAAACCTGT CCATAAGTAATTTTGTAAAGAAGGAGCAAGAGAACATTCTCTGCAGCACCTTCACTACCAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTCTTTTGCACCAAGACAAAGCAAGGCC
ESTD- BA511	29 A G ---	---	GGGCAACATAGTGAACCCCATCTCTACA/GJAAATAACAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAGCCCTGGGAGGTGGAGGCTG CAGTGAGCCAAAGATGGTGCCACTGCA



ESTD- BCL2	116 A G ---	---	AGCTGGATTATAACTCCTCTCTCTGGGGCGGTGGGGTGGGAGCTGGGGCGAGAGTGCGCGTT GGCCCCGGTTGCTTTCTCTGGGAAGGATGGCGCACGCTGGGAGAAC/A/GGGGTACGACAAACGGG AGATAGTGATGAAGTACATCCATTATAAGCTGTGCGAGAGGGGCTACGAGTGGATGCGGGAGATGT GGGCGCGCGCGCCCGGGCGCGCGCGCGCATCTCTCTCTCCCA
ESTD-BCR	69 C T ---	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCTCGCGCAAGA GA/C/TCAAAGAGGTGAGCTTCTGTTGCCGGAAAGGGAGGCGAGGTGACAAGCTAACTCTGCTTC AAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCGCTGGCACA
ESTD- BRCA1aa	119 C T ---	---	AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTTCGAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCA/C/TJGGTACCTGG TACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACA GAACCAATAAAT
ESTD- BRCA1bb	139 A G ---	---	ACTAATGTAGAAATCTGCTAGAGGAAACTTTGAGGAACATTCATGTACCTGAAAGAGAA ATGGAAATGAGAACATTCGAACTGAGTACAGTACGACAAATTAGCCGTAATACATTAGAGAAAATGTT TTTAAAG/A/GAGCCAGCTCAAGCAATATTATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA GTATTAAATGAAA
ESTD- BRCA1cc	126 A G ---	---	ATGCATCTCAGGTTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTTCGCTGAAATGACATTAGGAAAGTTCTGCTGTTTATAGCAAAAGCGTCCAGAA/GJAGGA GAGCTTAGCAGGAGTCTAGCCCTTCCACCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCA AGAAATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
EST51212 0	122 A C ---	---	ATCCTGAGCTCGCCATAAGCTTCTTGTTCTACTTCTCTCTCCACAAGCCCCAATTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCCTTGTGCTCCCACTCAATACA/A/CJAAAGGCCCT CTCTACATCT
ESTD-C1R	40 A G ---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCCTCCCTJAG/JATTTGCTCCGGGAAGCACATTCTAT CAA
ESTD-C1R	40 A G ---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCCTCCCTJAG/JATTTGCTCCGGGAAGCACATTCTAT CAA
ESTD-C6	31 A C ---	---	CCAGTCAGTTTGGGGACAGCCATGCACTGJAC/GCCTCTGTGTAGCCTTCAACCATGCATTCCATC TAAGCTCTGCAAAAT
EST20118 2	119 C ---	---	GTTCCGAATCCTCCTCTGAAAGTGGCCGGGTTTAACTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGGCTTGAAGCTGGGAGTGGGTTTAGGACGCGGGTCTGCGTGCATCCTAAGCTCT GAGGCAACCTCCCTTGAAGCTGGGAGTGGGTTTAGGACGCGGGTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	67 A G ---	---	ACAATCCAGGTACACATTCAGAAAGAGGAGGGGTGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA JAG/GGGATTCAAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC

ESTD- CB22	119 C T ---	---	GGCAAGTTTATTGATAGAGAGGAATCAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGGCAACCCATAGGG[C/T]GGATACAAAAG ACAGGCAAGGAAGGGTAGAACCATCAAGAGAGTAGGCTGGTACCOCAAAAGCAAGGAGGACCT AGTAACATAATTGCTTCAATTATGGTCTTCCCGGCTTCTCTCTCACACAC
ESTD- CB23	136 C ---	---	TAGAACCATCAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTCCCGCTTCTCTCACACATACAGAGCCCTACAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTTCCCTTCCAGAGGACCTGAAAAACGTGTCCCACCCGA GGTGGCTGTGTTGAGCCATCAGAACGACAGATCICCCACACCCAAA
ESTD- CB24	145 A ---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTTCCCTTCCAGAGGACCTGAA AAACGTGTCCACCCGAGGTGCTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCCGACACAGTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTACAGACAGACCCGACGCCCTCAAGGAG
ESTD- CB25	146 A G ---	---	GTTCCTTTCAGACTGGCTTCACTCCGGTAAGTGGTCTCTCTTCTCTCTATCTTCGCCGTG TCGTCTCGAACCCAGGCGATGGAGATCCACGGACACAGGGCGTGAGGGAGCCAGAGCCACCTG TGCACAGGTA/GJCTACATGCTCTGTTCTTGTCAACAGAGCTTACCAGCAAGGGTCTGCTGCC ACCATCCTCTATGAGATCTGTAGGGAAGGCCACCTGTATGCCGTG
ESTD- CB27	125 C T ---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCTGGTTCATTTGAGGAGTCTGTGGAGTCTGCTCATCTACCTGAC[C/T]TATCTTC TGATTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAAATGCT GCTTCTCCTGTTTCATCTGATGGAAGTCTCAACACACCATTTCCATACC
ESTD- D4S338	59 A T ---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGATATGA/TJATGTA TTTCTTAAACAATAAACTTGAAGTCCAAAATTACTCTTGATCCATGGACTGCAGATAAATGTTA TTTTAGCTGTGAGAAAACAATACTAATCTTGCAATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGA TTGCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTCATGCAAGTAG
ESTD- CYP2D6	61 A G ---	---	CAGGCCAGCGTGGTGGTGCAGGTACCATCCGGCAGAGAACAGGTACGCCACCACTATGCA/GJCA GGTCTCATCATTTGAAGCTGCTCTCAGGGTCCCTTGGCTGAGAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	40 A C ---	---	AAAAAACCATTTAACACCTTTTCAATCATATACACCAATAG/JATTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAACTTACTGCAATCTAAATGTCACTAGTAATGCAAGTTCAACAG ACAACITTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATACTGGATTAAATTATGCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T ---	---	CATCCCAAGCCCATCCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCGGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGAAAGGCTCTCTGCGGGCGGTG GGGTTGTGGCTATGTGGTGGTCTTGTGTAG/C/TJGGGGGCTTGGTTTCAGTTGCACCTATTGCGTT ATTGCAGATTGCTTGTCTTCCACCTTGAGCGAGCCTC

ESTD- D17S33a	75 C T ---				CATCCCAAGCCCATCTTAGCCACTGGCAATTTTGGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCTJACACATCAGGGGCGCCCTACCTTTGTAGTCCATGGAAAGGCTCTCTGGGGCG GTGGGTGTGGCTATGTGGTGTCTTGTGTAGAGGGGCTTGGTTTCAGTTGCATATTGCGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---				TTTGAGACCACCCCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCCTATCGTAATCCAGCTACATCGGAGGCTGAGGAGGAAATGCTTGAACCC/A /GJGGAGGCAGAGCTTGACGTGAGCCAAGATCACACCACTGCACCTACAGCCTGGGTGACACAGTGA GACTCTGCTCAA
ESTD- D3S11	44 G ---				AACTGATTAGAACCTGAAATACATAATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCAITTAATAATCCAATAAGTACACTGTAATAAGAAATTTAACAGAAATATCATTTGT TTATCAAACTATTATCACITATTTATTGGTAAGCCATATAAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---				AGGTTCCACATTATGCTGATTTTGGCTGATGTTTCC/AJGGGAGCCCTTGATGTCATCTGATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTATTAAITCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---				GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCG TGAGTCTTATTCAAACACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTTCCC AGAGTGAACATACTGCTCCTAGAACCCAGAGTCATACCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAATATAATAATCTGICCTTTATTGGGAAGGATGCGTGGT
ESTD- D3S2a	248 G ---				GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCG TGAGTCTTATTCAAACACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTTCCC AGAGTGAACATACTGCTCCTAGAACCCAGAGTCATACCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAATATAATAATCTGTCCTTTATTGGGAAGGATGCGGTATGT
ESTD- D7S399	83 A G ---				TGAATCTTAATTGCTATCTACAAAATGTATAAATCCTGAATCTGACATAGCCACCTCCATAGAT AACTGCTAGAGACCC/AJGJGCTCTCTACATCATCTTTTCAAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAAGAAACAACATGACAAACATTTTC
ESTD-DMb	146 A C ---				GTGGGACACCGAGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCCCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGGAGAGGAGGAGTGGGGAGGAGACA GAATGCTGATT/AJCTCTGGTGAGAACCAAGAACCTTCTGGCCCTGTGGGTAGGGGAGCTGCTTCCAAG ACCTCCTGATTTGAGGAAGGGGAGCAGCAGAGAGGAGAGAACAGAGT
ESTD-DMa	66 C G ---				GTGGGACACCGAGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCCCTCCAC/ GJTCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGGAGAGGAGGAGTGGGGAGGAGAGA CAGAACTGCTGATTATCTGGTGAGAACCAAGAACCTTCTGGCCCTGTGGGTAGGGGAGCTGCTTCCAAGA CCTCCTGATTGAGGAAGGGGAGCAGCAGAGAGGAGAGAACAGAGT

ESTD- DRD1	154 C T ---	---	---	TCCCCAGCCCTATCGGTGCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAC ACAAAACGGTCAGCACCCCAACCTGAACCTGCAGATGAATCTCTGCCACACATGCTCATCCCCAAAGCT AGAGGAGATTGCTCTGGGGC/TTTCGCTATTAGAAACTAAGGTAC
ESTD- DRD2	144 C ---	---	---	TCTGCCCTTTGTGCAGGAGGCTGCCGGCAGCCAGGAGCTGGAGATGGATGCTCTCCAGCACCA GCCACCCGAGAGGAGCCGGTACAGCCCCATCCACCCAGCCACCCAGCTGACTCTCCCCGACCCG TCCACACACGGTCTCCAGCACTCCGACAGCCCGCCAAACCCAGAGAAGATGGGCATGCCAAAG ACACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---	---	---	AAGACGATGGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGGCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTGAGGTGGC/TTACTCAGCTGGCTCAGAGATGCC ATAGCCACAGGGAGGTGCGTGATGCCAAGGGGCTTCTGTGAGGAGA
ESTD- ERB2	93 C T ---	---	---	TCCTTCAGGATCCGCATCTGCGCTGGTTGGCATCGCTCCGTAGGTGTCAGCGGCTCCACCAAGCTGG GGTGAGGGGTGGTGGTCAGTGC/TTGGGGCGCGTGCAGACCCACGCGGGCTGGGAGGACTTCA CCCCGCTCACCTCCGTTTCTCGACGAGTCTCCGCTCGTACT
ESTD- ETS2	43 A G ---	---	---	ACTCACAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGGCACC/AG/GGAAGCCGCTCTGGCGCCTG GCAGTCCGTGGGACGGATGTTCTGGCTGTTGAGATTCTCAAAGGAGCGAGCATGTCGTGGACACA CACAGACTATTTTAGATTTCTTTTGGCTTTTGCACCCAGCAAGCAATGCAAAACTCTTTTGAG AGGGTAGGAGGGTGGGAAGGAACAACCATGTCATTTCAGAAAGTTAGTTG
ESTD-F9	111 A G ---	---	---	AGATCCTGATGATTTTCTCTATTTTCTAAATGTTTACAGTTTGAAGTTTATAGATTTATGCCCA TGCTCCATTTGAGTTAATATTGTGTAAGTATGATGTTT/AG/GTCAAACCTTCATTTTTTTTTTCG ATAGGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAAAC
EST68787 5	144 A ---	---	---	CTTCCTATGGGATTTGACTTTATTTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAAG GAAGCTTGCAAGCTCATGACAAATTTGAAGCTGACAATTACACAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAACCTTGGTGTACCTTTAATTACAAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GODH	200 C G ---	---	---	CGCAGACCGGTGAGTGGGGTGGGAGTGGAGGGAAGGAGGAACTGGGGGTTTAGGGACT TTCCGGGTGACTTCCCGTTCTGTCTTGCAAGAAAGGCGGGAGAACACAGAGCCAACCTGGCTAA GTGTAAGGACCTCTGGTCGCACCGTGTGTTCTGCTGCCCTGTTTCACTGTCTGTCTGCGCGAGTTC/ G/GACTCTGTCCCGAAATCCGAGAGCT
ESTD-GCK	88 A G ---	---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTCTGGTCACCATGAC AACCACAGGCCCTCTCAGGA/AG/CACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCGAGCGCGCCTGAGCCCGAGGAAGCAGGCTAGGATGTGAGAGACACAGTTC ACCTGCAGCCTAATTACTCAAAAGCTGTCCCCAGGGTCACAG

EST34088 2	62 A T ---	---	GTGGGGCAACAGTGGGAGAGAAAGGGCCAGGGTATAAAGGGGGCCACAAGACCGGCTC[AT] AGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTGTGGACAGCTCACTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCAAC[AG]GGCATCA TTGAAACCAAGTTTTCGGTCAAGACTTGAATTCAGGTAAGTGCATGGTCCCTAGG
ESTD-HT2	154 G ---	---	GGGCTAAATTCGAGCAACTTTCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTACAGTTTGTACAGAGAAATAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTTCACATCCCTGGGAGTTAATAGTGCATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTTCAAACAAGACACCTT
ESTD-HT5	149 C ---	---	AACACAAAGCCCCAGCGAGAAATGAACCTCGGACCCCTGGTTACAAGACCAGTCTTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGGTTTCTTCTTCTTCAITCTATAGATTGATGTTATGCTCTA GCATTCGGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCTCTACAAAATGAAA ACATTTCTGCTCTGTAATCCCTCGAAAAGTTCT
EST37382 5	124 A G ---	---	CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCTCCCTTGGA CTTTGAGTCAATTTGGCTGGACTTGAGTCCCTGAACCAGCAAGAGAAAGAAAGG[AG]CCCCAGA AATCACAGGTGGCAGCTCGCTACCGCCATCTCCCTTCTACGGGAATTTTCAGGGTAACT ACCCAGTGGAGCCCGCTCATTCGACGGTCTTGGCAGGAGTG[C/T]CTGGGAGAAAGGAAGATG TTCCAGGGCACATAGCTTAGTGAGACTC
ESTD- IGHV4-6	43 C T ---	---	TTTACTATTTCAATGGATACAGAAATGTGGGAGTCACTATATCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATTTGTGAGTGACGGGAGTGGTGGATCCGAGAGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAACGGAGTTGAATATAAACCCA
ESTD-IL1A	110 A G ---	---	CAAAGTAAGCACCCCAATAATGTTAGCTATTACTATCATTAATTATTATTTATTTTATTTTGG AGATGGAGTCTGGCTGTCAACCAGGCTGGAGTGCAGTGGC[AG]CAATCTCGGCTCACTGCAAGCT CTGCTCTGGGTTTCATGCCATCTCTGCTCCCTCAGCCTCCGAGTAGTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTACCCGT
ESTD-IL1B	99 A G ---	---	CCACTTACAGATGGATAATGGGTACAAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCCTC[AG]GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---	---	TCCAGGTGGCTGGACCCAGGCCCAAGCTCTGCAGCAGGAGGACGTGGCTGGCTGTGAAGCATG TGGGGTGAGCCCAAGGGGCCCAAGGCAGGCACTGGCTTACGCTTGCCTCAGCCCTGCCTGTCT[AG] TCCAGATCACTGTCTTCTGCCATGGCCCTGTGGATGCGCTCTGCTCCCTGCTGGCGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGACGCTTTGTGAACCAACACCTGTGCG

EST45311 0	151 C T ---				GCCCTCCTCTCTCCAAATTCGTGCCCTATAGTTTTCTCTATTAAAGTGAACATACATGCATCTTTTAGT GGATAGATGCACACAACACACAGCCATTATGGGAAGGATCCACGTGTGGCCATATTGTAACA CAITTTCTGCAAAATC/TJACCCTCTTTCAATTAACAGCCCTTATCAATGGCCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTGTAAT
EST65258 8	80 A G ---				TGCCCCATACGCGCGCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACAGAAAT CCAGTTATTTCC/TJG/CJCCCTCAAAATGACAGCCATGGCCGCGGCTCTTGCGGGCTCGTCGGG GGGACAGCTCCACTCTGACTGGCAGATCTTTGTCATGGAGACTTGAGGAGGAGGCTTGAGGTTGGT GAGGTTAGGTGCGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	26 A T ---				ATGCAGGATGAAGGTGGACAGGAGG/TJGAGGGCCCAACCTGTCAATCCAGGGCCTGCAGATGTG CTGGACTATGGGTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	149 G T ---				ATACTAGTACAAAGTGGTAATTTTGTACATTACACTAAATTTAGCATTTGTTTAGCATTAACCTAA TTTTTCTCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAA TTTTTTTCTCTC/TJG/TJAGTGCCAGTATCCAGAGTTTGGTTTTTGAAGTACATGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTTCTGCTTGGGGTTTTTGGTGCAATGCA
ESTD- KRT10b	183 C T ---				CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAAGTCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGC/TJTGCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT10a	133 A G ---				CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAAGTCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTGTCTTTTAAATAGT TCTGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8b	231 C T ---				ACCTCACCCCTCCCTAGCCCGTGGGAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGCGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCTATCTCTCCCGTCTCAGGTTTACCA/C/TJGTCAACATTGACACA
ESTD- KRT8a	21 C T ---				ACCTCACCCCTCCCTAGCC/C/TJGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGCGCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCTATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
EST75099 6	82 C T ---				CACCTGTGTGTAGATCTCCTCAGTGGCCGCTCTACTGGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA/C/TJGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCCCACC CCTTCTCTTGGCGGCTTTGAGGTGGG

ESTD- LF79	142 A G ---	---	GGTGATTTGAGGCTCAGTTAATATTTCAAATGTAAACGTAGCAAAACGTCATTGGTATTTAGA AAAAATAAAATTTCCAATATGTAGTGCTGTATTACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCA/GGGAGGGCTTCCCTTACCACCCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCCAATTAGGTGAACATGGCTTCGAG AGAGTTG/CJACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA A
ESTD- LMP2	35 C G ---	---	TACACACTTTCCTTACCCATTCACTGAAAACGACTC/GJGCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCCAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTCAGCTCTGGCCTGTCTGCTGCCTGCA AGGGTTTGTCTTAATCTCAATTCATGTCTCTCATCTTTAG/CJTAGCTGTGGGGTTTGTGTG TTCTCTGTTTGTCTTAGTATCTGACTACTTTTAAATTATAAAAGAGATGTATCTAAACAAATAG AGATTGTTATCAGAAGTTCACAACATTTATTAATAATTTTTCACCTG
ESTD-MOC	45 C T ---	---	TTGTCAGGAGTGTGCTGATGCTGCCTCCCGAGCTCTGTCCTAGC/CJGAACTTCAGGACAACGTGC AG
ESTD- METH	118 C T ---	---	CATCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTCCAGGGTTTGGTCAAGTTGCTGATTACCC/CJGGATTTTCTGACG ATCTTCAACTGTAGAGCATCTGGTTCCTGTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAACCT/GJACCAGATCCCACAGACTGATATGGCTGGT
ESTD- NFKB1	107 A G ---	---	AACATGGACTTGATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAGAGAAA AAATTTAAAGGGGTACTTATATCCACACTGCACACTGCCT/GJGCCCCAAACGCTTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTGAAATTCT GAGAAAACCTTCTTTTAAACCTCACCTTTGTGGGGTTTGTGAGAGGTTATCA
ESTD- NPPA	45 A G ---	---	TGTCCTTAGGCCACGCCCTGCTTGTCCTCCCTGGCTGTATCTT/CJG]GTACTGCAAAAGAGAACACA GACAT
ESTD- NPPAS	202 C T ---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTCTGCAGGCATATAGAATTTGGT GGGTTTCTTTTATGTAGGTGATATTGGATACCTTTTGTGTGATTATATATAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGCTTGAATAGTAGTATCTTATTTAACCTTGGCAATAGCATTG C/JATTCCTCTGTGGTTTATAAAAAAT
ESTD-PAI1	100 A G ---	---	GCCACCACCCACCCACCCAGCACACCTCCAACTCAGCCAGACAAAGTTGTTGACACAGAGAGCCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG/GJG]GTACGCCGTGTATCATCGGAGGCGCCGGG CACATGGCAGGGATGAGGGAAAGACCAAGAGTCTCTGTGTGGGCCCAAGTCTCTAGACAGACAAAAACC TAGACAATCAGGTGGCTGGCT

ESTD-PAR	120 A	---	---	CTCTTCAGGAACCAACAGTCTCTTACCAACACGACGATTATGCTGTCGAGAGGTACAAACCCGTAGA
ESTD- Per/RDS	74 A G	---	---	ACTTCTTCTAAGTAAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGGCT
EST68308	29 C T	---	---	AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTCCTTCTTCTTCTTCTGTTCTAGAACGTTTCTTAG
5				GACTGGCAGTTTAAAGCTTACATTAGCTTCTGTATACCCATGCC
EST54045	39 A G	---	---	ACCTACAGACGCTGGCTGGATGGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGCAGGGCTGGCTG
6				CTGGAGA/A/GGAGCGTGGCGGAGACCTGGAAAGGCT
				GGAAAGAGATTAAAGAGCTTGAATTGGATTCGAACTTCTGTTCTTGTGAGTGTGGAAGAGTTTATGTC
				TCTGCCTGAGTTACAACAGAAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT
				GGAGAAGTAGACTTTAAAGGTAAGAAAGTAGTATTTTTTA
				GGAAATTAATAATATTTAAATACCTCCATTTGCTT/A/GTCCCTTTTAGTGAAGATGATACCTGC
				AAAAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA
				TCTGTTAAGTAAGTACTGTTTGGCTTGGAAATGGATTTTAAATGTGACITTTATCAT
ESTD- PXMP1	88 A G	---	---	ATGAAACATGGTCTTTAATTTATGATATGTTGTTATAGCTATCTTAAAGGGCTTCTTTTTTTTA
				ATGCAGAAAGAGGGGAAAAA/A/GGAGCGAGCTGTGGTGACAAAGTGTCTTCTCAAGGCTCATAC
				AGATTCTGAAATCATGTCCTCCTAGAACATTTTGTAAAGAGTAAAGTCTTATGAAATTTATAATCTT
				CCCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGCTGCTGGAGAAGAGCGTCCCGGAGACCTGGAAGG
				CCTTCTGGAGAGTGAAGAAGCTGGCAAGGGCAACAGGTGGAGCGAGCGAGCGAGCGAGCGAGG
				CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACT
ESTD-RDS	127 A	---	---	CCAAGAAACGTGGATCTCCCCCTCATCCCACTCCGAAAGTCTGAA
ESTD- s14544	94 G T	---	---	TTGGGAAGTTAGAGCTATATTAATACGGAATTAAGGAGGACACAGAGGCTTAATTGAAAAA
EST52908	45 A C	---	---	TATCCCAAAGTTGAAATGTCCTCAGTTCTG/TCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTA
0				ACCTCT
EST19590	55 C T	---	---	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGG/A/C/TGGTGGTCTGCAAGCCCTT
EST76136	39 C T	---	---	TGGCAATGTGAGATTTGATG
				AGGAGAAGCTGAGGAGGGGAAGAGAGACAAAGATGACATTGATGATGAAGATGTCT/GGGCTCAG
				GATGCCGGAAATGAC
				TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAACC/C/TGGCTCATACCTTTATCTATAGCCTT
				CCCCTAGTCTT
ESTD- SPTB	176 C T	---	---	TGAAACACCTGTGGTCCGGAGCCAGGTGTGTTTCTCTCTGGAGCCTGAGGAGTTTGTGTGTGTG
				CAGTCCCCCGCGCCACCTGCTGGTTGAGCCTGGACATACACCTTACCTCTTTGGCCCGGAGAGAC
				ATTTACCCACCTGGCCATGTCCTGGCCTGTTGTGCAAC/C/TCTCTGTGAAGACCCCAACCCCTGC
				CTCCCCCAACCAAGCCAGTTTCTTAGCAAGGGCAGGAC



ESTD-TAT	224 C ---	---	---	AAATGGTCAGGACCCGTATCCACAAGAAGTGTACCATTTTCATCAGGGCCATCAGTTTCATTTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATTTAAATGACTTTGTTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACAACTTTTCTCCAGTATGGATGGGATGATGATGGGGG GAGAAGCAATTTTAAATAGGACCCATGAGACACATCA
ESTD- THRb	125 A C ---	---	---	TGGGGCTTTCTCCGGCAGGGTAGACTTCTACTTGGCTGTGATTTCCTCAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATC/A/CJCTTCAT CCACACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCCTGTGAGCTTCTGGATTCTTGTCCACCCGCAACAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCAGTATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAGAGGTCATAAATATTGATGTCGTAA CATGGGTGTGATCCATTTTCATTTGGCCATAGGTCCCTATGGGGATGACA
ESTD-TYR	122 GT ---	---	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCACTCTCTTATGCATTAGTATCACA AACCACCTGGTTGAATATAATAGATTGAGTTAATACTGATTTTCTTTCACITTTATACCTTCTTCT AATACAAGCATATGTTAG/A/CJATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C ---	---	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCACTCTCTTATGCATTAGTATCACA AACCACCTGGTTGAATATAATAGATTGAGTTAATACTGATTTTCTTTCACITTTATACCTTCTTCT AATACAAGCATATGTTAG/A/CJATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C ---	---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCCAAGACACAAGGTTCACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA/C/TJGAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 C T ---	---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCCAAGACACAAGGTTCACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA/C/TJGAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T ---	---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA GGACAC/A/GJTGATGCTGGAATCACCAGAGCCCCAAGACACAAGGTTCACAGAGACAGGAACACCA GTGACTCTGAGATGTCA/C/TJGAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G ---	---	---	ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAGGACAGCCAC/GJTGCGCGGGATGGCGCGGGAGTTTC TGGTTGGCGCCACGGCTGTGGCCTCGTTGTGAACGGTAGCCTTTGGGGTTCGATGCCTAAACCTTTGT TTCTTGCCAAAGGAGGGCGGSGTGCCATGCCCTGAGATGTAGATGGGCG
ESTD-VWF	36 G ---	---	AGGTAGGAAGCAAGAGATTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGCTCCTTTGG TCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACCACTCTCACGTCAAGCCTCAGCACCAAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTATTTATCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAGAGTACCAG/C/GJGTGGTGGGA AGGAGTGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAG
ESTD- TNFα	152 A G ---	---	TTCTGTCATCCTGTCTGGAAGTTAGAAGGAACAGACACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAAAGACCCCTC/GJGAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATG CTTGTGTCCCAACTTCCAAATCCCGCCCCCGCGATGG
ESTD- TNFα	88 A ---	---	TTCTGTCATCCTGTCTGGAAGTTAGAAGGAACAGACACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAAAGACCCCTCAGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATGCTT GTGTGCCCAACTTCCAAATCCCGCCCCCGCGATGG
EST52418 6	113 A G ---	---	CAAAATACAGGGTCAACTGCTATGATGTTTGGAGCCAGTACCCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACT/GJAAGTGAAAACGTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACTCTATTGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAAGTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC/GJGGGCTGGCTTATCAGCCTCCAGCCCGAGACCCCTGGCTGCAGA CATAAATAGGOCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCCTGGCC COGGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAACTGGGCCCCCATGCGGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAGGTCAACTCTTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG/JTCTCTCTC CTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGAGCAGCAGGAGCAGGTGCAGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTTGGTAGTCCAGTGTGACTCATCCACAATGATTCTCCAGTGCCTCATCTTGTCTCGAGTTT CTCTGCCATGTTGCTATTGACGAGCGGACCTGTCCCAAGCAGATGATTACCATTTTCCACAGTGGT CCC/GJTTAAAACATTTCTATGAGCCAGGAGAGATACGTATTCCTGCAAGCCCGGCTATGTG TCCCGAGGAGGGATGAGAAAGTTTATCTGCOCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T ---	---	AGACCTCAGTTTCTCTTGTAAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGC/C/TJAGCA CTGGTCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACAGGTGGAGAGAAATTTGAAAGGGCA TTGGAATTGAGAGCAAGAGACAGATATTAGAGCTGGGAAATGTGG
EST39852 8	106 C G ---	---	CGGCTTCCTCCAGGTATTGTTGCAGAAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCAATTTCTTGAGGTGAGTACACCTTCCCACTCTCTTAC/GJGGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTTGGAAAAGGCCCTGTTTCCAGTGTAAAGGCATGCAAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---	---	ACCTGGTGTGCTGGTGTGAGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCCTGGGGCCCGTGG TCCTCCTGGTGTGCTGGGTAGTCTGGAGTCAACGGTCTCTT/GJTGAAAGCTGGTCTGATGGCA ACCCTGGGAACGATGTGTCCTCCAGGTGCGGATGGTCAACCCGGACACAAGGGAGAGCGCGGTTACCC TGGCAATAT
EST36027 2	120 A C ---	---	AGTGACTTCCAAGGAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAATATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGG/CJAAACCTGAAAA AGGCTGCTATTCTACAGGGCTCTAATGATGTTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTGTAGATGGCTGCTCTAAAAAGACAAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112 A G ---	---	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTCTGCTCAGCTTTC/JGJGGGTTCAGAGGTGAAAA GGTGAACAGGTCCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97 C T ---	---	TGAGAGAACACCTAGTCTCCATCCTTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTCTGGACCTGGAACA/C/JTGGACTTCTTCTACTGCGAGGACAGAACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTTGACCAAACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---	---	GCCGCAATGCCCGGGAGTTTCTCCAATGTGTGGAGAAGGCCCTTAGAAGACATGTTTGATGCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCACTTCTCTCATCATGAAAAAC TGGGAGGCCGGGCAT/JGJGTGCTCATGCCTGTAAATCCAGCATTTTGAGAGGCTGAGGCGGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAAACAT
EST12274 0	135 A G ---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGAT TACATAAAGAAAGTCAAGTGGTTTACTCCTCATGACCAATATCTTCCCTCCTTAGGATGAGGTG A/GJTAGTAAATGACCCGATGGGGTCAGAACTGTTCTGTCAACCATGGAGGATACTATAACTGTGAAGA TAAATTCAAGCCACAGAGCTTGCCAGATC
EST76807	91 G ---	---	ATGCTAAGGGGATCGGACATGAAAGGACCTGTGAGCCGATTGCTCTATCTCCAGGGCCCTGTCATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACCACCTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T ---	---	TTACATTTGTGGATTGTTCTTTTGTCTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAAGTTTGGCTTGGCTGCCTGTGCTTGTGGGATATTTGAAAGAGATTC/TJTTGCCAGTCCCATGTCTCTAGAGATTTCCCAATGTTTCTTGTGAATAGTTTCATAGTTTGAGGCCCTTAGATTTAAGTCTTTAATCCATTJTGATTTGATTCTGTGA
ESTD-RYR1	109 A G ---	---	CTTCGTGACGGAGGTACGTCCTCCGCTCTTTTCATGGACATATGGATGAGTGTCTGACCATTTCCCTCTGTGACAGTATGACACGCGAGACTTGTCTACTATAG/A/GJGGGAGCTGTGTGCACTCATGCCCGCTCCCTGTGGAGCTGGAGCCACTGAGAATCAGCTGGAGTGGAGCCACCTGCGCTGGGGCCAGCCACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCCGAGG
ESTD-WT1	70 A G ---	---	AAGACCTACGTGAATGTTTCACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCGTGCAGGATGTGCG/A/GJCGTGTGCTGGAGTAGCCCGGACTCTTTGTACGGTCTGCGCATCTGAGACCATGTGAGAAACGCCCTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST44438 7	100 C ---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGTCATGCACGCTTAACCTCTGCACCAAATGGCTCCAAAGGCCCGTAGGGAACTGGGGGATCTAGGGGATGGGTAGGAATGGCCCGAGCCAGTCCCGCGGTGCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGGACACAGGAGATGGGC
ESTD-PBDA	103 A G ---	---	TGGATGAG GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACITTCGAAGGA/C/TJGTCCTGCTCGACCTAAGCGGAGAGCCTCAAGAGCCGAGCGGAGTGGG
EST12839 3	122 A G ---	---	CCCTCTCATGCCCAGATGGAAATTCACAGTCCCTTACAGATCTGCCTAACCTGTGACAGTCTAAAGAGTCTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAA/A/GJCTCTACCCGACGCTTGCTCGCATACAGACGGACAGTGTGGTGCAACATTGAAGCCCTCGTACC
ESTD-CTLA-4	48 A G ---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCTCCTAACATCTATGTACTGGATTATCTAATGAACACACAGCAGCTTACTCCAGAG/A/GJTCGAAGTCCAAGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACCTTGAATGTATTCAAC
ESTD-ACE	96 C T ---	---	TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG ATGGCTTGCCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCTT/GJCCAGGACCTGGCCCTGCACCTCTCTGTTTTTCTCTTCTATCCCTGTCTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGTACTGGCCAGCAGCCGAGGCATGCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCCAAAGCCAC
EST54419 8	88 A G ---	---	GATCAAGCAGTGCACACGGGTACAGATGGACCAGCTCCACAGTGCACCATGAGATGGGCCATATACAGTACTACCTGCAGTACAAGGATCTGCC/C/TJGTCTCCCTGGCTGGGGGCCAACCCCGCTTCCA TGAGGCCATTGGGGACGTGCTGGCGCTCTCGGTCTCCACTCTCGAACATCTGCACAAATCGGCCCTGCTTTCTGCTCCTAATTGAATGATATTGTGCTGTGGGACCTGAGCAGCTTTATGGCACAATGATCACTATTTCTTGACCCCTACTTAC/A/GJATCCTGGGAGATGATTTGGGTTTAGCGTGGTCTGATGTGTCTATATAGTCCCAAGTGAA

ESTD-PS-1	99 A G ---	---	---	GGGAGTAAAACTTGGATTGGGAGATTTCATTTCTACAGTGTCTGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACCAAGCCTAGCTTTCGTAGCCATATTAATGGTTTGTGCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	---	GGCTGCCAGGGTTCCGTGGAGGGGCGCTAGCCGGGGCCCTGCTGGCGCTGGGGTCTGGCCACC GTGGGAGGCAACCTGCTGGTACATCGTGGCCATCGCCCTGAGGACTCCGAGACTCCAGACCATGACCAA CGTGTTCGTGACTTCGCTGGCCGCGACCGACCTGGTGATGGGACTCCTGGTGGTCCGCGCGGGGCCA CCTGGGCG
WI-567b	48 A G ---	---	---	TCTCACACTGACCCCTTACCTTCATCCTCACCTCTGCTGCCCTTGGTTCAGAGCCCTCATCTCTTTA CAGGATCCGCCACAGCATCCCACTGATCTGGCCTTAGGCTCTCTTCTCCAATCCATTTCTCAAAG GCTGCCACTGTGATCTCCCAAAGGTGATCTGATGCTACCATCTTGCTTCAAGCC
WI-801c	58 G T ---	---	---	ATGGAAACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCACACATCCCTTTCTGTAGATGG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCCAGAGAGTTAA CATTCTGCCACCCCTC
WI-801b	58 G T ---	---	---	ATGGAACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCACACATCCCTTTCTGTAGATGG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCCAGAGAGTTAA CATTCTGCCACCCCTC
WI-1099b	76 A G ---	---	---	GAAATTCACCTATACAAGAACTATTTCTCTAATTTACATTAGTCTCATTATCTGAAATATTAT TTTTACAAGTACCTTTGATTATTTTGGTCAATTTGTAACGAGAGATTACAATATCAGTAACGC TGTTCAATTGATAGTGTATCACAATGTCTAAATACITTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTTGCTTTAAGTTTA
WI-2529	71 C T ---	---	---	AGGAAATGGCTGATACCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGACCTCT CAA[C/T]TCTTAACCTGCTGCCCTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTTATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---	---	---	TAAGGCCCTGTCTTCCCCAGAGGCCCGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCTTATGAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAAGACTTTTACATTTTAGAC AGG[C/G]AGCAGAAAGCAGCAAGGAGAGAAAGGAAGT

WI-2625	98 G A ---			GGCAGTCCTGGCTGAGTGGTAGACAGCACTGAAGGATGGAGGAGAGAGAGAAACAGGCAGAA GCACTGTGGTAGTTAACAGGCTTATTTAGGA[G/A]CAAAATGATGATACCTCCCTGAGGACTCGCAG AAATTACCAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATTCACCTGCAGGAGGAAAGCCA GCCAGCAAAG
WI-2924	54 G A TAGG	TGACCTTCCTA GTCTCTCTTA	GCCTAAGTGT AATCAGAGGG	TCTGTTGTCATATTTCCCTCTTTGACTCTGACCTTCCTAGTCTTCTTTATAGG[G/A]ACCCTGTGATT ACACTTAGGGCTACCTGGATTATTTAGAACAAATC
WI-2939	72 G T GTGCCTTT	GGCTTGCTCA	CTTGTGAGGG AAGGTCTTG	CCATTGTTGAGGTTGGGTGGGTCACTTGTCTATCCCTCGCACTCAACAAAGTGGCTGTCTCAGTGC CTTTG[T]CAAGACCTTCCCTCAACAAGATGTCTTTCCATGCTCCCGTGTCTTTGAAAATTCGACT TTATCCTGAAAAACTCAGCTGCAGTGTATCTCCGGTATAAAGCCACTCCTG
WI-3203	99 G A AGACGAG	GGTTATGCCGC	TCAAGTATTGC CTTGTGTGG	CTTGCTACCATGCATTTACAGCATACAACCCCTCAGTGAATGCCGTAAACCCCATTTATAAAACAT CTTGCCATCGAAGGGTTATGCCGCAGACGAG[G/A]CCACACAAGGCAATACITGAAGTGACTTGGA GAATAAAGATTGTTGGATGGATGAAAGCAGAGAGAGATGCTAAAAGTGA
WI-3473	101 A G GCCCTAGGGA	AAGCATTTTA	CCTGATGTCAC CAACATTTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTTGGGAGATAGTTGGTAGAGCCCTGTTTGA GATTGCAGAGAGGAAGCATTTTAGCCCTAGGGA[G/T]AGAAAATGTTGGTACATCAGGGCT ACACACTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATGTCTGGCTCCCC
WI-1796b	29 A G ---		---	ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATGTCTGGCTCCCC
WI-1796	29 A G ---		---	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCTGCAGAGTAGGAAAGAGATGGGTGAGT AGTCACATTAGGTATTTCCAAATAA[C/T]AAATGCCCTCTGAAAAATATCTCTCCCATGTCCCTGTC TAAATATAACATTTTCCC
WI-4360	93 C T AAATAA	GTAGTCACATT AGGTATTTCC	GAGAGATATT TTCAGAGGCAT TTT	GCTGAGCTTTTGGCAGAGCCAGGACAATTCAGCTGCCGATTTTATAGATTCTGCAGCACTGCAA CAGGAACCAAAATCAGTC[C/T]GGGTAACTGAGAGTGGTTTTCACACCCAAA
WI-1959b	87 C T ---		---	GTTGTGCCCTGTAGCAGACACAGAGGCA[G/T]GAGGAAAAAGCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTG
WI-1973b	28 A G ---		---	CTTGAGTATGCGTGGATTTTGGTATACACAGAAATGGGAGAGCTGGAACATAATCCCCCATATACCA AGGGACAAATTGTATCTGTTCTACAAATTACAGTAGGAGACATTATGTTCCATGACAAATGGTAAT TTTTAA[C/T]GACAGTTTTTAATTGAGTGAAATACCATAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGCCTATAAATAGC
WI-1980b	140 C T ---		---	

WI-2015b	190	A G ---	---	---	TGTCAGATAGTCGGTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCACACAAGACTAT GTGTGAATCGTCTATTAGGGTTTCTATAAAGTCTACATGGTGCCTTTTCCAACT[A/G]CATATACCTT CTAATACCATAGAG
WI-754b	49	C T ---	---	---	GAAGGCACAGGAGAGATGGCTGTCTATCTACCAGCCAGGAGAGAAAGC[CT]ACATTTATTGGTAA TCCTATAAAGTGCACTCTTTAAATTTGTATTACTTTIAGA
WI-754	22	T C ---	---	---	GAAGGCACAGGAGAGATGGCT[CT]GTCTATCTACAGCCAGGAGAGAGCCACATTTATTGGTAA TCCTATAAAGTGCACTCTTTAAATTTGTATTACTTTIAGA
WIR-1b	56	A G ---	---	---	AGGCAATCAGACCTACAGAAGGAACCCCAATAAAAACTCTGATGATCGTACATCC[A/G]TGGCTG GAGGTGATGCTCCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56	A G ---	---	---	AGGCAATCAGACCTACAGAAGGAACCCCAATAAAAACTCTGATGATCGTACATCC[A/G]TGGCTG GAGGTGATGCTCCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72	A G ---	---	---	TAATTTTAAATGGGGCCAATAACACAGTACTTATCTACAGGATTTCTCTAAAGGCTAAATAAGAA GAAGT[A/G]TCTAAAAAGTTATTAGTCTCAGAGCCCTACACATTTCTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69	A T ---	---	---	TAATTTTAAATGGGGCCAATAACACAGTACTTATCTACAGGATTTCTCTAAAGGCTAAATAAGAA GAATGATCTAAAAAGTTATTAGTCTCAGAGCCCTACACATTTCTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47	T ---	---	---	GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCTGTCTACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-5g	209	C ---	---	---	CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGAGCCACAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5f	196	C ---	---	---	CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGAGCCACAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5e	194	C ---	---	---	CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGAGCCACAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGTGGCTCTATGGAAACACAGG TTTTACGTCCAG

WIR-5d	191 A ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCAG
WIR-5c	177 C ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCAG
WIR-5b	159 A ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGT AGGTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACAC AGTTTACGTCAG
WIR-5a	37 A G ---	---	TAACCCGTGAACCTTTGTCTCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGCTTGGGGTGGGGCAG
WIR-6	63 A C ---	---	TTGCTGACTATT[C]AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-7	12 C T ---	---	GGCGTCTATGACTATCCTGGTCACTGATTTGACTAATGATTCTG[C]TGCCCTTG
WIR-8	46 C T ---	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACTAAAGTTGTCAGAAGAGGTATGA[C]GJCTGAAG AAAGAACTACTCTCTTTTGACCAATAAATACAATTGGGAAACACTGGAAACCCATGGCTTGATTACT GACAAC
WIR-2	56 C G ---	---	TGTCCTTGCTTATGCCTGCCTCTTTGCTTGGCAGGATGATGCTGTCATTAGTATTTCACAAGAAGTA GCTTCAGAGGGGTAACTTAACAGAGT[G/A]TCAGATCTATCTTGTCATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCAACCCAGTGAATGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAT GTACAGTGGTCTTTTCAGAGTGGACTTCTAGACTCACCTGTTCTCACTC
WI-7069	93 G A ---	---	GGTCATTCTCTTTTATCTGTCAGGAGCCAGCTGCTGACTTATCTCTGTTCTGTCATCTCTCCC CCACATACCAACTCTTCAACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A T ---	---	CACACTGTTACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTCAGAGCAGCAATACAAAAAGTA TTCATGAAGMATGCATAATCTCTGAAAAATTAAGAAACATCCCT
WI-18612	37 A G TGC	TTGATTGCTG CTTGCAAT	



WI-18517	87 C T	CAGGAATCAG CAGCCTGA	TGTTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCTCCATTTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA[C/T]TGTGCACTTGTCACAAACAACACTGACTGC
WI-18668	76 C T	GGCGAAAAAC TAGGCAAAA	GCTAAATTAAA CTGCACTTTT GC	CGATTGACAACCTTTTATTTTCAACCTTAGGTAAACAGTCCAAAATCAGGTAGATTGGCGAAAACT AGGCAAAA[C/T]AGCAAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGTATGTGGAAAGGAA GGTGAGATTCCCTCCTACT
WI-18680	75 T C A	GCTGTCACTCT AGCATCTGGA	CCTCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT[C/G]CTCCGTTGTATATTCAGGAGGGA
WI-18704	99 A C	GGGTTCTCCGA GGGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTTCTGTGCGAGACCAACACCAAGGCGAGTTGGGTTGAAGGAGCC CTTGAGGAAACACGGGTTCTCCGAGGGGTAC[C/G]CCAGCAGGGCCTTCAGCTTAAAGTCG
WI-18673	29 A G ---		---	TGTGGCAACCTTGTTTTAATTGCAAAAC[A/G]ACTTAAATTTACAGCACATTCAATAATGAACCAAC AGGAGAGTGTGCTGACTTTGTAAATATGAATATATAAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAGCGCATACAAGGAAG
WI-18640	121 T C	GTGTTGGGTG GGG	GCAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTTATTGGAGGTTAATCCTATTAGGATATGAAAGGATTCAGCAACGATTGAGATT GTGTTCTCAGCGAGGGCTCGGGCCAAAGTCTGGGGTGGGGGTGCAGAGT[C/G]GTGCTCTTC AGTGGATTTCGGGACC
WI-18533b	91 T C ---		---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCAATTTTTTAACTCCCGAGATTTCTCTTTATTT TATATTTTCATTTTTCATCCTAA[C/T]TACTGAAGCCATTTCTTTGGTTAACTTAGA
WI-18533a	59 T G ---		---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCAATTTTTTAACTCCCGAGATTTCTTTGCTTTA TTTTATTTTCATTTTTCATCCTAAATTTACTGAAGCCATTTCTTTGGTTAACTTAGA
D11734	83 A C TTC	TCATCTGATAC CTTGTTCAGAT	AACCAGGATA AGGCTACAAC ATT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTTTTCATCTGATA CCTTGTTCAGATT[C/A]AAATAGTTGTAGCCTTATCTGGTTTTACAGATGTGAAACTTT
D49493	159 A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGGC	CAGGACTTGTGTGCACTGCAGACACAGACACAGCTCATGGCAACATCACTGGGGCCAGAGAG AGCTGTCGCCAGTGCATCATTAGGGGTCTTTCAATTGCTAGTACTAGCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATTTA/TJGCCCTGGCCTGAAAGTGGCCCATCATACCCACTGTT CT
EST10030 7	98 T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTCATAGAGGAGACCTAGGAGGAGTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCC[C/T]CTCATCCATACCACCCTGCTGATTG
EST10052 2	24 G A	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG[A/GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCAATAACCTGGTGGGAAGTCAATCATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGGAA A

EST10605 2	118 C G	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	---	CTTGGCGTAATCACAGTTCTGTATTATACAAAAA AACAAATTTCCAAATGGACAGGAACCTTAAATTT AAAAAGAAAAAGATCCC
EST11048 0	61 T G	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	---	CATGTGTCATCCCATGATTGAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTTTGJAA ACAAATCTTTCTGAAATTTAGCTTATGAACTCATTACACTGCAAAACCAGAGAAGGAGCAC
EST11260 8	101 G T	---	---	---	TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTGTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T	---	---	---	TTTGATGGAGAAATCCGAGGCCCTGCCAGCATCCCCACCAGTAGATTCTTTGGACGAAGAAAAATCCT TCTGTGGAATCAGCTTTACCGCCTTTCTCATCTGCTGGTGT[C/T]TTCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G	CCAACCTACTT TGGAGCCCT	---	---	GAATTCCTGGGTATTAAATAGCGGGTGCACAGGACACATAGGAAGAGCATCCAACTACTTTGGAG CCCT[A/G]AGGAGTTTATAGAGAAAGCTGGAGCCGGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGGAGGAAGGAGTGGAA
EST11772 6	74 A G	---	---	---	CCAGGAATAAAAGAAAAAGAGTCAGAGGAAACAGCTTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA[A/G]GACTATTTCATTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A	---	---	---	CTTGCCATTATTTTGTGCATGTTGTTCTTAAAGGCTTGGAAGATAACTTGAATGTGGGAAC ACATAGATCCCAGA[G/A]TATTAAAGGGGCTGGAAAAAGTAGCCCTTAAGAC
WI-16644	42 G A	CAATAAGCAG CTCATTTTGAT TAC	ACTTCATGAAT TTTACTTTCATG TATACC	---	AGAGCAATGGTGCATCTCAATAAGCAGCTCATTTTGATTAG[G/A]GGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAGCCCTCCACAGAACTTTCATGCACCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST12005 9	56 A G	TTGTATAATA ACACTCAGTA CAAAGTCTGT	GGCTGGTCACT TCCTGGAT	---	GCCTAGTAATTCCAAAGGAACATGTTTGATATAAACACTCAGTACAAAGTGTGTA/GJATCCAGG AAGTGACCAGCCCGACGTCGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAATC
EST12055 9	32 T C	---	---	---	GTGGAAAAATTTTATCTGTTACGCTTTCC[T/C]ATTATATTTATCTTGTCTTGATTTTCAGCACCC CACCCGATTTCAGGCGAGTCTTCTAAACTGTGCCCTGTAGCTGTAAAAAGTCTTCT
EST12492 1b	95 A G	---	---	---	CCCCTAGCAAAATGACTTGGAGTTGTGTCCAAATACCAAGTTACATACTGTGGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[A/G]GGAAACGCACAGCAAAATTGACGATGCAGCTTTTAA CCTTTTTA
EST12492 4	25 A G	---	---	---	ATCTTGAGGTTTCTGGGCCGTGTCAG[A/G]AAGTGACATCTTTTACTTACCACAGGTGAGGAACCCCTAT AAAGAAACTGTGTAGAAAAAGATATCAGGTGACACTTTTTTAAAGGGCTTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATACTAGGGAGAAAAACCAAACTGGAGGCAAGTCCACAGGTCCACACTTGTGCA[C/G]CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAAATGCTCAGGGGGAATGACCATTTTTAAGGGCCATGTG GTCGTCAGGCGAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGATGTATCGGTAAAGAAAATAGGAATGCATATTTCAACTCACTGTGCACAAA CAGGTGTTTATTATCCCAAATGACAGTGTGCTGAGAT[C/G]GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCCTTCAATTTATTCATTGTTTCAAACACTGTCTAGTACCAACATTTGCCACCGGCG[C/A] /GTTGAGAAATACAATATTGAAGAAGAGTCACTGCTGCCCTCTGGAAAAATCAGAGTATTGA
EST12817 9a	22 C A ---			TTGGGTTCTCCAGGATCCAG[C/A]CTCGTAGCTGATGTCATGAGGTTCTCATCCATGCTCCACGG GTTCTTGGGAGTGACCGGATGGGAATCCATGTTGCTTTCGCTACTCCATCAGGTCATTGGC
EST12941 8	23 T A ---			TCTCAGCTTCCAGCTGACCTGCA[T/A]CAACAGCCCAAGTTATTTACCAGAAATTTGTTTGGGTTTCA ATGATGTTTAGCTTTAATACACTGCACCTTGTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGCTCCTGT GGGTCTC	AGGATTCATGAGGCTTTAATCATAACCTAATAATACTGTTAAAAACAACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGGACACACATTCTCTCTCTCATATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTTGTTTTCTTAATGAAGCATAATAACAGTTAAAAATTTCTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCTAAATCAGTCTTCTAGGGCCACA[C/T]GGAGCAGAGCAGCTTCCCACCCAAAG CACCTCTGAAT
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCCCTTTTAAAAATTTAATCGCTTTATACAATTTGACACCAAAATAAAATGCAC[A] /GJTATTTAAAGTTTACAATTTGAGAAGCTGACACGTTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTCTTC[C/T]TAGGATATTCAGCTATAATCA CCTACATTCCCTCCACAAATATTTCTGTGTGTGCGCAGGCGAGTCTCCTCACTGCCCCATGAATAGCC AGTCTATTTCACACT
EST13226 6	74 T G ---			AACTGTTTACTAACAAGGTGCTTTAATTTGAAAAGCATTGAGGAAATAAAATTAATGAATAGTCT GGCCATT[T/G]GACTAACAGTTCTACAAATTTACATATCCGTCACCTCAGATGAGCATATACCAAG TCAGAGGAACAAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG ACAGAGA	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTTACACCAACTTCCGCTCAATATGCAGCTCAGATGTGAGAG ACGC[G/A]TCTCTGTACAGGAGCGGTACTGTCTCAATCCCTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	ACAAGAGGGTT TGACAAAAGA	G	AAAGATATAAAAACAACACTCCCATCAGTAGCAATACAAGGTTATACATTTTAAACCAGATTTTCTCAGG CCTT[C/T]TTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAACCCCTCTTGTATATAACCA

EST13278 2a	51	A G	CTTCACCGAA CAATATTTAG	CATATCTTGG GTGGTGAGAA	TTCCGAGAACGTTTTACAAGCTCCAAACCTTTTACCAGCAACAATATTTTAGGAG/GJATTTGAAATTAT TTCTGTAGTTCTCACCACCACCAAGAATATGACAGCTTG
EST13282 0	99	A T	CCACACATTTG AGTCCAAGA	GATGGAAAATTT TGAGGAAGGTT	GCTCAGTAGATGAGCAATTGACCAAAATATTTAGATAATACCTGTGGGAAAGTGCTGAAATTACTAGCC TGCCTGAGAAATCCACACACATTTTACGTCCAAAGA/TAACCTTCTCCTCAAAATTTTCCATCTCCCATCAGA
EST13290 9	39	A G CTT	CAATTTT TAGA AGTTGGGTTT	AAATCACTTCA TGGAATTTCA	AGCTCATCTGCAAGCAATTTT TAGAAGTTTGGGTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTCAGTTACTTAAAGACCTAAAGAGCAAAAGTGATATCACATCACATATTTTGT
EST13518 2	45	C G	---	---	ATGTGTTGGCTTTTGG
EST13522 8a	66	A G	---	---	GAAACATCTCCAGTAGTATTGAGGTTAAATGATTACGACATTTA[C/G]ACTTTTAAAAATTACCTCA ATGTTCTCTCGGAGTCGTCATAGTTTAAATGACTTCTGCACCTTCTCTATAACCTTGATTG
EST13568 6	69	T C	---	---	CAGTTGGTGATTCTCAACTAGGAGCTATTTTGGCCCCCATCCCCACCCGCGAGTGCTGGAGAC/A GJTTTTGATTGTACAACTGCGAGAGGTGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13785 0	101	C G	---	---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA[C/G]GCACACAAGGAATAAGGGAGAGGAGGTTTCGGTTAGTTGAGGGAGAGAAAGTTGGAAGCA
EST14038 1	25	A G	---	---	TTTCAAGCTAAGTAAATGGT
EST14083 7	23	A G	---	---	AAGATTACGGACCATAAGAACTGCCCCCGACCCACCCATACACACACAATTTTAGCAGGTAAAAACCA CTGAAAGGAACAAAAGTAATGACTTTCTTGAACAAA[C/G]TGATTACGAAAGTGAAAGGCTACAGGG
EST14221 5	42	T C	GCATGCTAGA CAGAGGCATT	AAATATTTTT AAAAGA	TGATTACTA
EST14812 2	50	A G ATA	CAAGTCAGCTT CTACATTCTGA	GGAACAAGTC TAAAGATTTAC TTAAATCCCAT TATGTACT	CCTCAACCATCTGTACCCGAGCC[C/G]CAGTGACCCGGGACTTGCTGCTTCCCCATCCAGGCCCTCT CCTATCAGCATCCGCTAAGGTCAGTCAGCAGGTG
EST14815 3	128	A T	ATACCTGGTT	CGGGAANAACA GTACCGGAA	CAATGGTGTCATGTGAACATATA/GJACCTATTTCATAAAAGTTAAAAATAATCCCTTCTTGCATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGACCCGAACAGGAGGTAGGAGG
					AAATCAATGCATTCTTGTGGCATGCTAGACAGAGGCATTAT[C/T]TTTGAAGATCTTTTAAAAAT ATTTTGACTTGTCCCTTCACACTCATTTTAAATTGT
					TTACATTAGTACCAAGGATGCCCTTTC AAGTCAGCTTCTACATTTCTGAATA/GJAGTACATAATGGG ATTTAAGTAAATCTTTAGAAAGTCCCGAGTTTGCCTTTTCTAACATTTTTCATATCAGGTGAAAAACAAT
					TTTTTCATATGGGTGATT
					TTTGTCTGGCAATACATAGTGGCAATGCAGCGTGAGTTGCGCGCTCTCCCCACTGAACCCAGTAAT TCACCAGACAATGGCGCACCACTTAAATAAACTTGGCCGTCATCACCCACCATACTGGTT[A/T]TTCG
					GGTACTGTTTCCCGTA

EST15420 6	109 C A ...	...	GGAAATAGCTGA AACAGAGATA TTATTCTC	TTTAAACCCAAAGACTTGTAGATGTCAGGACTCCGATCATTTTCTCTGCCCTATAGCTTGGATATCTTA ATCTCTCCCTTTTGTCATATAATCATATAGCCAAAGGACTC/A/GGAATTTTGGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48 G C GGA	GGTTTGCCAT G A CACAAGC	GATAAGTGGATG TTCATTATCC CTATAA	GTCACCAAGCCTTTTATTAAAGACGTGAAAAGACAAGACAAGAGAGGA/GC/JAGCAGAGAAATA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTA
WI-16739	57 G A	GGTTTGCCAT G A CACAAGC	GATAAGTGGATG TTCATTATCC CTATAA	AAGGATTGAAAACATACCTAGATCATATAAAATTTGTGAAGGTTTGCCATCACAAAGC/G/AJTTATAG GGAATAATGAACATCAACTATCTACAGCTAAACCTAATGAAGACCAAAATTCCTCCAAAGT
WI-16782	96 C T CACTGTAAGG TC	GGTTTGCCAT G A CACAAGC	GATAAGTGGATG TTCATTATCC CTATAA	CTTCTCCTTCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGG/C/TJGATGGAGGAACAGAAAGATAGAAGAAGTTTGGGGT GCTGATGAAATGTGGGG
WI-16783	64 A G G	TCCTGAGATGT CTTTACCTGA	CTGCTTGGTTC AATCCTTATTA G	AAAAATGTAAACCTTAGAGGTTGCTCTTTTGTGTCACTTTTCTGAGATGCTTTTACCTGAG/A/G CTAATAAGGATTGAACCAAGCAGTATTTTTTAAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C ...	...	...	CAGGACTTAAGGTCAATTTTGCCTGGAAAGACTTAACTAAAGGTGAGGGCAACATAGGAT/CJTGTGA CAGCACACTGGACCAAGGAGTGTGAAATCGTCACACTAGCGTGCCAGCCCTTTTTCCTGGC TGCTCGCTCCAGAGC
EST16088 8	89 G C ...	...	...	GGTTTGAAGACGCAGCTTATCTCCACCTGCCACTGGGATCTCATTTTGAGAGCTGTTTGTGAGGC TTTTCCAGAAAGGCCGCTG/CJGGGTTTTCTGAACCTCTATGGGCATTTTAGAAT
EST16089 9	96 C T ...	...	...	CGTCTGAAGTTTTCTTTTATCACAAGTCACTCAATCCCTCGGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC/C/JAAGAGCCATCCCTGCCCTTCTTTGCT
EST16100 1	24 C G ...	...	...	ATCCAGCTGTGAAGGGACAGAGGAG/C/GJGTAACACACAGTCCATTATAAGGGGTGTGCACATTCCCA GGGCTCCAAATATGCAACATTTGTTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTGGCTC
EST16104 9a	83 A G ...	...	...	TTCTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAAGTGATTGTCAG CTGGTCTCCAGGGA/JGTTGGCCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C ...	...	...	ATGGTAAACAAATCAGTTCAGGTTTTTTTCTGAACAAATGATCCTTTGGCTTTCCCGTGGCATG CTCCTAAACAACTAAACCAACCCCTCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G ...	...	...	ATGGTAAACAAATCAGTTCAGGTTTTTTTCTGAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCCTAAACAACTAAACCAACCCCTCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ---			AGCCAAATCAAACGAACCTCTATCAAAACACACAAAGGCCTAGAGGAGAGATT[C/T]AATGAACGT AAATAATTCAAGGCAATTTTGATCTAAAGCATTTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ---			CATTGGTTGGTAGGGAAGATAGTAGTGCAAAATAAAATGTTAAACAGCAG[G/A]AAATGGAA TTATAGCTTTCTTTTCATATAGGAATTGAAATTTATTACTGAGGTGATAGGCAGAGTAGTA
EST16183 2b	59 A G ---			GCAGGTAACACTGTGGTTCAACAGTATTGTTCTTTTCATAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACCTGCTCTCTGGCCCTCTCTGTTTCATATTTTATGTCACTGTCTTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---			AATCTTAGGCTCTTGGCTTTCAAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTCCGATTT CCCCAGAGGAAAAGTCAGCATCATAAACACATGGTCACATGCTCACGCACATGGTGTC
EST16229 2c	52 T C ---			TGTGAACCTCGAATTCGCTTGTCCAAAGTCTGAGTCACAGTTTCA[T/C]TGGGAGT[C/C]CCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGAGGATCTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
EST16229 2b	45 T C ---			TGTGAACCTCGAATTCGCTTGTCCAAAGTCTGAGTCACAGTTTCA[T/C]TGGGAGT[C/C]CCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGAGGATCTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
WI-16816	124 A G TGGGGTTA	GGAGCCATTGT	GCCTAGATTTT GTTCAGGACAG	CAGACTTTCTCACAACCTATTGGCTGGAAGTCTTAAAGGCCAAGCAGGAGCCATTGTTGGGTTA[A/G]ACTGTC AGGGAATGGGTATCAAAATGCTTAAAGGCCAAGCAGGAGCCATTGTTGGGTTA[A/G]ACTGTC TGAACAAATCTAGGCTC
EST16269 5b	49 G A ---			GCCACTCTCTGTGGCTGTCTCTGTCCAGCTGCTGCCAGTGCACAG[A/T]GGTCTAGCCTCATGG CAGAAGCATTTTAGCCCAACTCTGTGCTGCTCCACTCTCTCTCTCCGCCGCTGGGGCTCACCACC TCTTCTCTCTCAATC
WI-16824b	83 G A ---			GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTGTTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTGCTG	CAGCTTCTGAC TTCTTCATAAG AA	GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTT[C/G]TCTTATGAAGAAGTC AGAAGCTGATAAACGTGGGCTTACACCTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---			TTGCTTTTATTAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTTATTACAAA AATGGCTTCCAAACCATTAATAATGAACTT[C/G]GGAATAAGAGCATAAACGGAAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCCT	TATAATCCATCTCCAAACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCAAGACCTGTGCTTCAATTTTCTGATAAIGGGAGAAATCTGCTCTTTATGTA

WI-16879	79	C T	GATACAGCC ATATTTCCCA	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAAACTCCTAGGGATAAAGATATAAATCCAGCACAGCATATTTCAGATACAG GCCATATTTCCCAIC/TATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCCACCCAG
WI-16882	99	A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTAGGTGGGAGAGACAATTTCTCCCTTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGTCTCTGAC/GGCGATTTACCTGACATGTGTCATCTCCCT
WI-16888	70	G A	GCAGGTTG	AATGTTCTGAA TTGACCAAAAT TAA	GTAGTAAATGTTCACTACTACCCGGGGAGAGCAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC[G/A]TTAAATTTGGTCAATTCAGAACATTTCCAAAT
WI-16905	75	C T	GTGTTCA	GTCTACTCT TCTAGGCAGTG GG	TTTGTGTTGTTATTTGGCTCCCAACATCAGAACATAAAGTTCCATGAAAACAGGAACCTTGGCCTGTG TTGTTCA/C/TCCCACTGCCTAGAGAGATAGACA
WI-16910	74	G A	AA	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTTCATCTCAGAAAGATAAGATGGCG CTAGAA[G/A]GTATCTGTTATAGAAACGATACTTCAATTTGGGCTGAACCACTGAAGGT
WI-16918	93	C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAATAAACTACCACCATTTCTCTGCTACACAGAGCACTAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACAGCAC/C/TGATGCCACTTCTGTATCAGGAACCTTAACTGACAAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127	A C	GGAAAGCAGA CCTGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGG/A/C/CCA CGGGCAATCAGATGAGATG
WI-16947a	58	C G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAG/C/GJACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGGACCA CGGGCAATCAGATGAGATG
WI-16966	43	T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTACTTTAAATGCACACTACATAACAACCTAATA/T/CJTTAACTTGGTCCAATTTT AGTATAACTAATATGAGTTTTTATCTGATACTGATACTTGAATGCAATGGCAATTAAA
WI-16995	55	T C	GAGCAGTAGA GACTGAGGTA	CATGTTGATTT CCAGCGGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAATAGTATTT/CJACGGCTGG AAATCAACATGCCTCTTCTCTGTGAAGTTGTCAGCATGGAGCTGAGAGGGTGAGTCAATCT
WI-16992b	60	T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTG/CJCCCTCATCTGAGAT/GJGTG TAGGACTGTAAAGGAATGTGTTTGGGGTTTAGGAA
WI-16992a	46	G A	AAGCACCAG AAGTACACTG TC	CACATTCCTT ACAGTCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTG/CJCCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTGTTTGGGGTTTAGGAA

WI-17010	23	T C	TTCAACAGGA	AATAACGGT	ATGTTTCAACAGGAAAGCCATGTC/JATGACATTCAAACACCCGTTATTATTAGAAAGCTCATTTAAT
EST17127	74	C T	AAAGCCATG	CA	TGTTTAAATGCAGACAAAAATCAAGGCTAACTAAAAGCAGATCCAAATGACCCAGTGATCAACCTAGA
9b			CACTCGGCAC	GGAGGGCAGG	GGTIOCCAGC
			AGACAGAGT	GGTG	ATTCCGTCTCTCAACAGCATCCAGGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA
			AATCTCTTAT	GGACTATGGCT	CAGAGTCT/JTJGGAGCCATGGGGCACCCCTGCCCTCCCCAGGCTTCTTAAGTAACAACCT
			CATCTCAAGCC	TATTCAGTGAT	CACGCGTTCAATTAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC
WI-17040	94	T C A		G	GAGAAATCTCTTATCATCTCAAGCCAGTTC/JCATCACTGAATAAGCCCATAGTCCOCAGTCTCGTTTTCC
			GCCAAGGGAT		AAATCTTCTCATATGT
			TAACGTATAG	GGGATCCCT	TTGTTTGTGTTTGTCTCTCTCTGCCAAGGGATTAAAGTATAGGTC/JTCTTAAACAAGGGGATC
WI-17044	47	G T G		TGTTAAGA	CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCTCGCAGAATGGCAGGGAATCGAAT
			TGGACTTGTCA		CAAAAGAAAGCAAGTG
			GCCTATAACT	TGTAGAGTAG	GCATGTGTGGAGCAGATCTCCATGTGAAGCCAAAAGTGGACTTGTGAGCCCTATAACTACTCT/JA/G
WI-17021	62	T A ACTC		TGGCAGCTGC	CAGCTGCCACTAACTCTACAGGCACAGTAACACTTTATACAGGAGCACATGCCAAAGTGCCTGG
			CCAGAAAGGA		GAGGTGCCAATAAAATCAA
			AAAGCATAAA	CCCAAGAGAC	TGTAAAAAATGTAGACATGGGGAAAAAACAATTCGTAAATCAACATGTGCTGTTTTCTACTTCOCGGTA
WI-17065	90	T C CTT		AATGAAATCCT	CCAGAAAGGAAAGCATAAACTTTC/JAGGATTTCAATGTCCTTGGGT
			TGTACAGCCA	GAGATGTTGAA	
			ACATCACTGTT	AATGTTCTGGA	TTCATAAGGTTGTACAGCCCAACATCACTGTTTT/JATTCAGGAACAATTTCAACATCTCAAAAAGA
WI-17066	32	A C T		A	AACTCTGCACCCATTAGCAGTCACTCCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86	T G ...		---	TGCTGACTGTCATGACTTAGTAAGGCCATCACAGTTGCCAGAACATCTACTCAACTGTTCCAGCAT
WI-17104b	108	T C ...		---	AACTCTCTACACAGGCCCT/JGCTACATAGGAGTATATTTGGCCAAAGACTCACTAGAGTGATT
					CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCTGATGCTTTGCGAGCTTTCCCATTCATTCCA
					AAATCAGAAAGCAGTCAGTGGCCCCGGTTCAGACGGCTTC/JTCTCTTTGTTAAGAAATTA
WI-17114a	37	T C	TTCCATCAAG	ATAGCAGAGTG	AGCGTCCAACAGATGTTCCATCAAGGACTTTGTTTT/JGCTCTCTCACTCTGCTATTTATAATAC
			GACTTTGTTTT	AAGAGAC	AAGTACCTCCCAAGGCCAGATGCTCTAAGTGCTAAAAGAAAGACTGCAGCCACAATCAGAGTTACAT
			GATGAAATTC	TTCTCAGAATC	GGGA
			AGATAGTCTTC	CTGGAAGATAT	
WI-17150	76	T G CTCIT		G	CGTGGCTGGACTAAGTGCTCTTTCCATGTGGACACATCTCCACTGAACAGGATGAATTCAGATAGTC
			CATTTCITTTGT		TTCTCTTT/JGICATATCTCCAGGATCTGAGAAAGGCCCTCTTTGCTGCTCTAAATTT
			AAAATAACAA	CAGAATCTTGC	GAAATCGAATACGTCCATTTCTTTGTAATAACAATAACGTTT/JAAGGCAAAAAGCAAGATTCTG
WI-17163	43	A/G TAACGTT		TTTTCCTT	TAAACCAACATTGGAAAGGGGACACAGGGGAGGGGAGGAAAGGCCAGATTTCACACGGTTT
					CCTCCACATCTGCAGACAAA



WI-17178	127	T C	GGACTCCTCA TGAGGAGC	CCCTCAATTTT CAACTGCTTC	AGCAATGTCCCTCCCAATTCATTAGCTATGATGGAGTTATCAGTTTCATTTTCAGAGCGAATTACTGG GGCAGGGGGTTTAATATCTGTGGTTTAATTCAGTGAGGACTCCCTCATGAGGAGCTC/CJAGAA GCAGTTGAAATGAGGG
WI-17180b	81	C G	---	---	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACCTCCCAAGTCTCGTCGCACAG GCTTCAACAAATTAC/CJ/AACATCTTGCCCAATTTGTTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17180a	47	T C	CACAAAAATA TAGAGAATCC TGCA	TGGACGAGAC TTGGG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACCT/CJCCCAAGTCTCGTCGCA CAGGCTTCAACAAATTACCAACATCTTGCCCAATTTGTTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17156	54	G C	TGTTCTCTAAA CTTTAGATATC TCCCA	CAAGAAATAT ATATTTGATTC TGTGGAA	TGAGGTAGCAGGGCATTCTTAAGAAATGTTCTCTAACTTAGATATCTCCCATG/CJTTCCACAGA ATCAAAATATATATTTCTTGTTGGAAATTTAAATGTTCTTAACATCTGCCTACCATCCACCTCAAT TAATATCTTG
WI-17149b	79	T C	---	---	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAAACATCTCATGCACGTGCGTGGAA ACCCAAATGTCAIT/CJGTGTATGAACACAAAAGGATGGGAAAGAACACATTTCTCACA
WI-17149a	48	C G	CAAGTTTGA AGGAGGAACA	CCACGACGTG CATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAAACATG/CJTCATGCACGTGCGTG GAAACCCAAATGTCAITGIGTATGAACACAAAAGGATGGGAAAGAACACATTTCTCACA
WI-17197	67	G A	GCAGAAAGTAG CTGGGGCTAC	GGTGAGTGGT GCATACC	ATTTGCTATGTTGCCTGGCTGGACTCCAGCAATCCTCCTGCCTCAGCAGAAAGTAGTGGGCTAC/G /AJGTAATGACACCACTCACCTGCTATCAGTTTCGTTTAATAGAATATTGACTTTTAGATGCGCA
WI-17198	38	A C	TCCCCTTTGTC CCTAGTTT	TCCATTTGTC ACTGAGAAAT	TGATTTTCAGTACTTTTCTCCTCCCTGTCCTAGTTT/CJTAATTTCTCAGTGGACAAATGGACAA ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC TTC
EST18753	27	C T	CTACCCAGGCT GGTCTCAT	GGATCGCATGA GCCTGA	TCGCTATGCTACCCAGGCTGGTCTCAT/CJTCAGGCTCATGCGATCCTCCTGCCTGTCAGTGGCTGG GATAAGACACAACCTGCCACCGGCTGCCCTAGGAGTAGTCTTAATGCCTGATGGTGGG
WI-17108b	74	C T	GCCATTCAGTC TCAAAAGTAAA CA	AACTACGATTT ATCATATGCTC CC	TTATTTTAAACATAACCAAGATGCACCTGGTTTACATTTCTGTTGCCATTTCAGTCTCAAGT AAACAC/CJ/TTGGGAGCATATGATAAATCGTAGTTTAAGGAAGCCATAGCACATTACAGAGT
EST19067	41	A G	---	---	ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCA/CJGTGGCATTAAAGTACATTCAACT TTTTGAGCAACCCGCCCATCCATTTCATCTCCGTT
EST19067	40	A C	CGTGACCATTT AAGGGTATAG TTC	AAAAATTGAA TGTAATTAATG CCA	ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTTC/CJAGTGGCATTAAAGTACATTCAACT TTTTGAGCAACCCGCCCATCCATTTCATCTCCGTT
EST19125	28	A G	---	---	CTGTTTCTCAGAGATGACACTGCCAACAC/CJTCACAGATTTGCATACAATACAGTTATGTATTGGC TATTCACAAATTACAGTAGTGTTTCTCTGAAAAA

EST20824 8	115 T G	AGTCGGGAGT T T G C T G A T T G	AAGATTTTATC T T G G A C C C G A	GTGTGAAGCGGAGTTTATTATTCAATCAGTCTCTGTGAAAACCTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTGTTGTTCTGGGTCCAGATAAA ATCTTAGG
WI-17347	50 A G	ATCCTCAGAA C T T C T C A G C C T	TCAAGCATCCA C T T G T G C T A	TTGGTTAAATGATGCCAGATGGGTGCACATCTCTCAGAACTTCTCAGCCCTAGTGAGCACAAGTGG ATGCTTGAAGAACTCAGTCTTGGAACTCAGACAGCAATGGAGCGGATGTGAGTGGGACCA
EST21904 b	128 G A	TTCATATGGCC A T T T T A A T A A G T G	GGCAGGTGTTT A G A A A G C A T	TGATTGTGGTCTGGGAGCAGGTGGGAGTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTTCATATGGCCATTTTATAAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT C T G G C A T T C T T	TGGA AAAACA G C C C C A C	CAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGCTGGCATTCTTTTTCGTGGGGCTGTTTTCGAAGGCACA
EST22197 2	78 T C	AATTATCTGC T A T T C C T G C C A	ACCATGAAGG A T G C G G T	GTTTAATGATCACTCACCAAAATCCACAGGAGAACTCTTAAATGTTTACAAGCACCAATTATTCTGCT ATTCTGCGCATTCACCGCATCTTCATGGTAGAGTATCACAAAGTAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T C	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCATGGTTTACTCTATTCGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A G	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCAGTGTAAA CAGTAGCATTCATGGTTTACTCTATTCGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T C	GGATTAGATC A T C T T T T A T T	TTGAATGCTAC T G T T T A C A G T G	TTTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATTCACATAAAAAATCCACCACCTGTAAA CAGTAGCATTCATGGTTTACTCTATTCGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19 A C	---	---	TCGAGGAGCTCTGAGGAGGACACCAAGGGACGTGTGTCCAGGGCCACCGTGCAGGCAAGTGTG GTCCAACTCCTCCTCCCTTTACAAAACCTCCAGCCTCACCCACACAAAACACTGGCTGACAGGCCCTCT TAAGCCTTTTAACTGT
EST22433 c	103 A G A A	AAGACATGTT C A C C A A G T G A	CAGCTTCAGCT T A A C T G A C A G A	GATGTTAATGACTTTCCCTTTGAGATATGATGGA AAAATATTCCAGGTACACATGGA AAAAGACATGTT CACCAAGTGA AACCAATCTAACCAAGAACTTTACCAGTTCTGTGAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC T T A T C T G C A C A T	AGTTTCAGTTT G C A T G A A T T T T	TATCCATTTCAAGAAAAAAAATGACITAAAAAATACAAATCTATCCAGAAATGGATCCTTATCTG CACAAGCTCCATTGAAGAAAAAAAATTCATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTGTT TCTACCCC	TTGCCTGTAA TTTGACTGTAA TG	GCCTTTATGCTCCTTTTAAACATCAAAATGTTTTATAACACACTTGATCCTTTTGTCTACCCCCA ATT/C/CATTACAGTCAAAATTACAGGCAATATAATAGGTCTAACAGAAATGCTTGCAATT
EST23021 0	108 T A	---	---	TTATTTCTCAGCTTACCATTGTTGTAATATCTCTGTACAAGGTTGTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAATTTTATTAATCTTTGCCTT/AJATGGTTTTGACAGTTTGTGCTTTCT T
WI-17387	55 C G	CCTTGCAGAT TGAAGAAAAA	GCCTTTGCCTA AGATTAATAGT AACTACT	ACAGAAATTTAACATGCAAGTTTCATTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAAGCCATTTCCTTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	OCITCCCCCTCC TGTAAGC	TTTTTGGCTGTCTGCAGATAGATGAAAAGAGAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACACTAGGCAATGTAGCTCCAGAGGCAG/C/GCTTACAGGAGGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG
EST23733 9	31 T G	GGCTGTTAGTT TTGTTTTGTT	TGCACCTTTAAA TCCCATCAAT	AAAGGCTGTTAGTTTGTGTTTTTCTT/C/GJTATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAAGCCCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGGCGC TGAAGAATACCCACCTAAA
WI-17470	83 A G	GTCCCGTCCCG CCAG	CCAGTGACGAG GOOGA	CTGACAGTCCCTGTGTGGGGGTGCTCATGTGGCTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTGCGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGTCTTGGTTGGAAA TACCATCAGCCTTCC
WI-17519	55 T C A	GTGTCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTAAAGAAATCTCACTACTGCAAAATGCATTTGTCTCTAGCTAAATGAATGCAIT/CJAGAGTATTG CCTGCAAAATATAATTGAGATTCTATTTTAAAGAGCTTAGAACAGTACATGGTGCAATAG
EST25356 3b	95 C G	---	---	TCTTTGATACAGGTAAACCAGTTTGTAAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTAT CAGCATCTCTGTGGAGAAAGCAGTGTG/C/GJTATAATGTCACATCAGGATTTCTTTTT
EST25356 3a	26 A C	---	---	TCTTTGATACAGGTAAACCAGTTTGT/C/JACATTATTGAGAACTTCACTGTATCTTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA/C/JTAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT ATTGATAA	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGATAAT/C/GATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCCCTGTG TAAACACTCG	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAAGCCCTACT TCCCTGTGTAACACTCCCA/GJATATTGTGATTTCTAGCTATAAGAAATGGGCCACTAAGTGGGTC

WI-17623	46 T C ...		---	TGTGGTTTAAATTTCCCATATAATTAATGTTGGGCACATT/CJGCATGTGCTTACTGGGTC ATTATATATCTTTTGTGAAGCATCTGCTCAATCTTTTGCCTGACCTTTGGAGTTTTTGGT
EST26419 1b			---	ATTTATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGAT/CJGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCTATGATGGCTGGTTCGAGGAGAAGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	46 T C ...	ATACAAAGGC AACTATGTGC	CAAGAAGTTTG GACTGOC	ATTTATACAGAGATACAAAGGCAACTATGTGCAG/CJAAACAATCTGATGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCTATGATGGCTGGTTCGAGGAGAAGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780			---	TCAGCTTTAAATTTAAGGGACATGTAAATAAAAGATGCATTTGACAGGACAGCAGACTAGTTCAAGC AG/CJAGGTTAGACCAGTAACAACAACCAAGAAAGCAAGTGCCTGCTTCCATCTTGGCTTTACCA CACTTACAACTGATACCC
EST26900 7	69 G C ...		---	TACTCAGTTTAAGGCAATTCACACACAGAGACTGTCT/CJGAGAGCGGGCACAGAAACAGACACC GTAGAAACACCACCACCATGTCATGACGGGGAAGCAGAG
EST27152 1	101 C T ...		---	CAAAGGATTTTATTTTTCCTTAAAGTAAATCTAGAAAATAGCAACCCACTGCAGAAAGAGTT CTATACTAAACATTTTCAATCATCTCTCTTCT/CJTTTACATGGTGTACTCTTTTCATGTACACAT CATCGAAACACAGACTGA
EST27504 0a		GGACTTGGCA CAATTTAATA ATT	GCTGGTGTGAT GCTACTGTAT G	TTTTGCACCTTGCACAAATTAATAATTTATC/GJAJATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGCTTTTCAGTATTTCTGTTACACATCTGTTAAACAAGAACCCATACATT GGTAAATTCATCT
EST27662 4		CACATTCTGTT CTCCAGTCTTG	TTATGGAATG GCTTATGTAAC C	ATCTTAAAGGACCATAGAAAAGGCCAGTCACATCTGTTCTCCAGTCTT/CJTAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTTCTTAGAGTAACACACACTCTTGTAGGAATGTTT
EST27788 3			---	ATTTTATTAGCGGTACAAATTCAGGTGGTAAAGGTGAAGGAAAGGCGAAGGCGAGGCAAAATACAT TATTGAGCTGAAAACAACTTTACATTTCAAGGAC/CJGIGCTTCCAGACAAGCCATGTAGAACCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4		GGAGTGCATC AGAACCCAC	GTGCAGAGAGG TACTCCAAGTA C	TCCTCTAAACTTCTCTGTTGGATCCCAGTACGCTGGAAGTGCATCAGAACCCAC/CJAJGTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369		AATAAAATTC AATCTGTCAC ACAATC	TCAAGAAGGCC TTATCCATT	TAAAAATTTGAGATACATTCCTCAATGTAAACAATAAATTTCAATCTGTACACAATC/GJAJAAATG GATAAGGCTTCTTGACAAATTTCTGCCACCTCCGTTTAAACGATCAGAACTCAATCTTATCTC
EST28036 4			---	TCCGCTTCCAAAGCTTTATTGGCAATATGCTCTAT/CJAJAAAGAATGATCAATCTGTTGCCCTCT AAGTCAATGGAAATGAAGAGCTGTGTCCAGGGACACACCACCGCTGCTGAAGGAGACTGCTGTTGTG TCCACCTTATTATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT TAAAA	TTTCTGCATT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTCTTCTTTAAATTAATGATGGTATAAAATAATGCGAGAAACATTAAC GGAGATGTACAGACAACAGACGAGACATGAGTTGTTTCTGACTGTGACACATTTGGTGAAA
WI-17724	50 T C	TGGGOCCTOOC TGTC	TGGGTTGGCAG TGTOC	AGAATTGGTCTAGTAATCGTTACAGATTTCGGTGATGGCCCTCCCTGCTC/CJGGACACTGCCAACCC CACAGCTGGAGGGGCACTTAAGGCACGTCATTTTGTGATTAGA
WI-17730b	68 T C	---	---	TGAGCCTGGGAGAAAGACCACAGAGTGAAGTGCTATTAGTTACATCATACCAAGTGTACATACTG TTT/CJACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGICA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGCTATT/CJGTTACATCATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGICA
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAAACACATTAAGCATCATTTGTCACCT/GA/GCTAACTCCT CAAATCAACAATACCCCTTTATTTTAGCCATGAAAAAC
EST29128 4	58 A G	---	---	CTTTTAGAAGGACACACAGCTCTGTTGGACTTAGGGCTACCCCTATTCACAGAGGTGCCJ/GJTTATTT TCACITGGTTACGCTGTGAAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTTGCTGGGGACACT
EST29912 3	103 C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTTCTCTG T	ATTTATTAGGTATCTGCTGTTGGGGTGGGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT/CJACAGAAAGAAATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATTTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAAAGTTAACTCACCATGAAA TTTAAACCTTCTGTACTGGCTTCACTGATGAGGCGAGTAAACTACATAGGGATAAAJG/CJAGCTCAGTA TCTGGAATCATGCTTCCTG
EST30223 2	99 A G	---	---	AAATAAATACATCATGGGGAATGGGATATCCATCCCTCAAGCAITTTATCTTTGAGTTACAAGCAA TCCAATTTACACTCTAAGTTATTTTAAATTTCCJ/GJGGATTTAATTTCTTCCCTAGTTCAATCTTGGGA GG
WI-16260b	86 G A	---	---	CTTTCCATTGGTATTAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAAGAAAGACCCAGA GTTTCACAATAAGGTAGC/GJATAACACAGGCTCACTTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTCCATTGGTATTAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAAGAAAGJG/TJACCC AGAGITTCACAATATAGGTAGCGATAACACAGGCTCACTTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTTCTTGTG/GJGGCTGTTTCTTACCCCAATATCATAGAAAT GTTGTTGCTTCTATAATGTTGAGCTTCAAAATCTTTTGTCTTAATCAATCCAAATGAATTACCTGAAT TTCTCCTCTTGTCAAAA

EST31951 4	87 C T	GGGTGTCCAG CCAACA	CCACCAAAAT CACCTOC	ACAGCCATTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTTAGCAATGACA TCGGGTGTCCAGCCAACA/C/TGGAGGTGATTTGGTGGGAATCTTATCACAAATATTCT
EST31968 8b	95 T G	---	---	CGAATTTGCTCTCTATTATTGATTCTAGTAATCCTAAAAGATTTGGGGCGGGTTACTATAAGT GCATTTTATAATGGGATTTCTGCTT/GJAACCTGCCCACTGATCTTACATGGGAAAGGTGCAAG ACAGTGGTACTGCTCCC
EST31968 8a	75 T C T	GCGGTTACTA TAAGTGCATTT T	TGAAGAATCA GTGGGCAGTT	CGAATTTGCTCTCTATTATTGATTCTAGTAATCCTAAAAGATTTGGGGCGGGTTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAACCTGCCCACTGATCTTACATGGGAAAGGTGCAAG ACAGTGGTACTGCTCCC
EST32063 2	103 C T	---	---	TCCATGGATGAACAGACGCTACCATGCCACATCCCACTCCCACTCCCGACCAGATGCTGTGGCCAGAC TGGCTTCCCCTTCCAGACCTAGCTGGCTTTGTAGT/C/TGTTCCAGGCCCACTTGAATAGCAACGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G	---	---	AAGGCTTCCAAGCATTCAAAGGCACTTGGGTGTTGTGCTCTAAGTTTCTGGTCACTGCAGCCCCC/A/G TCTGATTAGGGAGCACCCCAAGCCAGTAACAATATGGTCTTGCAG
WI-17800	29 C G	GGGAGCAAA GAGAACTCA	TTTCCCTACAAT TAATCCAGTC TT	TGGACATGGGAGCACAAAGAAACTCACT/C/GJAAGACTGGGATTAATTGTAGGAATAATTCACAG TTTCCACAAGTCAGAAGAGCTAATCCCAACCCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCTAAAGTCTG GGATGACTTTC G C	TGGCTTAGGT TCTACTTTGATG T	AACTGTCACTTCTAAAGCTGGGATGACTTTCC/T/GIATCTACATCAAGTAGAACCCTAAGCCAAT TCAGAATCAGAATCCTTTTGTCCATCAAAATCCAGCTAACTCCAAAGCTGAATTAATGTTCAATCT GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAAACAAAATCTTTA TAGTGTCCAAAGATAATTAAATCTTGGTTTAAATCTTTGCCAGCAAGCAATA/T/AJCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17860	121 T A	TTTGCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	CAGCAACCTTTTTTTTGTATAGCCTACTCTCAAAATTTGT/TATTTTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCAGTAACCTACCA
WI-17866	43 A T	TTTATAGCCT ACTTCTCAA ATTGTT	CCGTTGTCAC AATCACAAA A	GAAAAAAAAGTCAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCTCACACAAGCATGATC AATCGCCACGAGA/G/AJACTGGATGCCAAAGAGATGG
EST33301 4c	80 G A	---	---	GAAAAAAAAGTCAAATGTGTTCCCTTTTATGGGTGATGCCACCATGATTGCCTCACACAAGCAT/G/AJ ATCAATCGCCACGAGAGACTGGATGCCAAAGAGATGG
EST33301 4b	63 G A	---	---	CTATCCAAAGATAATTTATGCAGCGTGGTTTCAATACTAAACA/G/JGTGTAACAATGCAANTATT TAACAATAATACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAATACTTTTGCAA
EST33460 1	44 G A C A	AGCGTGGTTTT CAATACTAAA CA	CTGTATTTATT GTTAAATATTT GCATTGTT	

WI-17904	50 A	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACACAG/GJTACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACACAAACACAAATGA
EST34149 5	69 A	TGCCAAATAC TCAAGTGTGA GAT	AACTACTAGCG AGAACAACTA ATAAAATC	GTTTTTCTTTGAGTGACACAAGCTTGTTCATTTTGAGAAAAATGTGCCCCAAATACTCAAGTGTGAA T/A/GJGATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATTCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C	---	---	TGGGAAACATAAGTTAACTCAAGAAATATATCCAGTCTTTATGTTACTAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTC/AJACAAAGATTAAAGAAACTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98 C	GGACCATATG ATATATAACT CTCTAAAGC	CAGAAATTATG TGATAATACT CCTTCC	GGTACACAAATTTTAAATGGAAGGAACACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCCTAAAGC/CJTGGAAGGAGTTATTATCACATAAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118 A	---	---	CTCAGTAACCTCGGTGATAATCTGCCATTTATTGATTTATTTATGATAAAACAAACCTCTCATTTGTGA AAACAGCTAAGGGTGACATCTCCAGACCCCAACCACTGTCCCTGTAATG/AJ/CJCTGCTGAGAGTCC ACATTTTGGAAATCCAAAT
WI-17996	84 A	GTAGAGGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGGTGAAGCAGCATGAAACACATCTCCCAGGCCCTCGCAGT AGAGGCGAAGGGAACAG/AJ/GJCTGCCCATGTGCTGTCTCTAAAGACGCCACCCCTCAGGTTGATGT CACCTGTGGAGACCGGGT
WI-17136	33 C	---	---	ATTCTTTATAAAACACCATGTCCCTAAATGT/CJ/ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAAGACAGAGAAATGTGTCCT
WI-18041	24 A	---	---	GCCACTGAAAAAGGTGCTCTTCC/AJ/CJGTTTCTAACTCCCTGGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAAATACTTAATCA
EST35164 8a	57 A	CACAGCCTGTC GCCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTTCAAGCACAGCCCTGCCCCQ/AJ/GJCTTGA GATTCAGAAATCCAGAGGGTGTCACTCCTGGTTAGGTGCTTCTGTGACATTTCTCTTG
WI-18052b	67 A	---	---	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTTATGTACGAATCTTGGTTACACATCTTAGJ A/GJACAGCAGAGCTGCCTGAGGGAGGGTTGTGTTTAAATGTCGTATGTCATGCTCAGCACAGTGTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTTATGTACGAATCTTGGTTACACATCTT AGAACAGCAGAGCTGCTGCTGAGGGAGGGTTGTGTTTAAATGTCGTATGTCATGCTCAGCACAGTGTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G	GGGAGTGGGG AAGATAAA	CGTCACCTGTC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAAG/AJ/TGGAAGCAGGGGTGACG CATGCGAGGAGTCCAGACAAAAGACGGGTGATTTTGCTCAGGTTGGTAGCAACAGAGGTAATG

WI-18064	54	G A A G A	GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAACCCCTGTGGTAGCTGCTAAGCTGTATTTTCAGAG/GA/GAATGTACAC AATCATACCACCTGGGAGAAAGAGTAAGCACAGTGTCTATTAGGTGCCAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97	T C A A	GCATAAAATT TTCCAGTTGGT	CCCTCGGCAAC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATCTTGATCATGGGTGGAAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTTCCAGTTGGTAAGT/CJAGCAGGTGCCGAGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28	A C G T G T A T	AACCCACTAC TTACTCAGAGT	AAAACTAATA AGAACTGGA GGTTTT	AAACCCACTACTACTCAGAGTGTGTAT/CJATATTAAACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGTATATTTCTGTACTCAGAAGCATTTTAGGTTGCAAGGATATAA
WI-18080c	80	C T ---		---	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATCTACTATGCCGTG TTTGACTTTTAT/CJTTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080b	65	G A ---		---	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATCTACTATGCCGTG ATGTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080a	41	T C A G T C T C	GCAAATATCA ATATCAAACT	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTCT/CJTTGTAATTAATCTACTATGTC CGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18086	63	G A ---		---	GTGGGCATCCTATAAAAGCAGCCATGTGTGAACAAATGATATGCACAGAAAGCATACTCT/GA/ TGGCTTTGTTACACGGGTTTCTTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTTGA
WI-18115b	71	C T ---		---	AACTACATAGTATGGTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGACCTTTGGTATCCC TT/CJTTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115a	70	C T T T	TTAGTGTAACCT TTGGTATCCC	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGACCTTTGGTATCCC TT/CJTTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18136	78	A G ---		---	TTTTGAGAAGCACTCTGTAAAGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTTCTCTTA GGTAATTTTC/GJTAAGAACAAATAAAAGCATTTTAAAGTCCACTGCCGCTTAGAAACT
WI-18169	115	A G A G C T C	CCATCTTCCG	GAGTCTGCTT GTGCTCCA	GGCAAAATATTTTACATCACACCTGGAATCTGCCCAAGTCTTCCACTATGAAGGCAATCGTAGAG TGTCAGGAGGAAAGGTGTTATCCAAGCAGCCATCTTCCGGAAGCTC/JAGTGGAGCACAAAGCAGA ACTCGTGGGTAGATGGA
WI-18190b	26	G A ---		---	TGAAAGAGTCGACACAGCGGACACT/GJATCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGACATTAATCTTGGCGA



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WI-18190	62 G A	---	---	TGAAAGAGTCGACACAGCGGACACTGTCAATAGTGGAAACAAAGGATGAAGTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGACAAAATCAAGATGAGCTGGAGACATTAACTCCTGGCGA
WI-18181	100 A C	AAATATATAC AACACTCCCTT CAGATC	CGTTTACCAT TTGTTAAGCTT TTG	GACAGTGAACACATTGAAACACAAAATACAAACAAACATTAGGAACAAGAAATGTGTAATCCAA TGTGTGAAACAAATATATACAACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAACCGTA TGTTCTTGAAC
WI-18215	78 G A	AGCAGAGTTC CTGCCCTC	CCTCCCTCTCT OCCCC	ATTCATACAAGCATTTCTGAGTACAACTAGGGACAGGTATTTACAAAACAAATAGAGCAGA GTTCTGCCCTC[G/A]GTGTGCGGGGGAGAGAGGGGATTACGATTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTC
WI-18232	60 T A	TGTTGTTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGTT C	CATTTCCGAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A]GAA CCCTGAAACCTTTATTTTGAATGAAGTTTTGCTCAGAACTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76 T C	GGAAACTTG AGTTTGAGATC ACA	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAATGCTTAGATTTCTCAGTATTTATCAATAGTGTAAAGCTGGAAACCTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCACTTCTGTGGCATTCGGCAGAAAGTGGC
WI-18242	30 G A	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAACAG CTTTC	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACCTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119 C T	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]GAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]GAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T	AAATAGGAAA TATGGACTATC TTCAAA	TTTCATGCATCA TTTGTGCA	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G	GCTGTCAGCTA TTGTTATTCA AA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTGGATATGTGTTAGTGTCTATCATTAATTTGGAAAGCTGTACGCTATTGTTATTC AAAT[A/G]TATCTTCTGCTCCCTTTCTCCTTTTCTGGGATTCATTCGCAATGTTTATA
WI-1830b	66 A G	---	---	AAACATCTACAGCTGTCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGGI A/GTATGTAGGCAGTGAGTCAGGACTATGCAAAACCATATAAAATAAGAACATAATTTTTTTGTTGAT TCACA

WI-18330a	49	G A A A G A	TCCTGTAAAG AATCAGGGAT	AGTCTGACTC ACTGCTACA	AAACATCTACAGCTGTCTTAGGCCATCCTGTAGAAATCAGGGATAAGA[G/A]CTGAGGAAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCAATAAAATAAGAACATAATTTTTTTGTTGAT TCACA
EST37564 5	85	T C A G A	AAATTC AAGC CATCTACAAA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAAATGCTGGTTAGATACTGCATGTTATTTAAGCTAAAATTC AAGCCATCTACAAAAGAT[C/T]CTCATTTAGGCTCCATAGGCTGCAAAACACATCAAAAGGCATTAC TGTACTGGAGAGGACTGAG
WI-18327	104	G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAGGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAAGCAGTACCTC CCAAACAATGGTGAACACAGCTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGCGGAGGCAGA GT
EST37624 6b	102	G A ---		---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCA[C/T]GCTGA TGGCTGCAGTCCTCTGCGCTGCTGGCTCTCTGGACGGTTCAATCTACATGGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58	C T ---		---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCA[C/T]GCTGA TGGCTGCAGTCCTCTGCGCTGCTGGCTCTCTGGACGGTTCAATCTACATGGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89	C G	CCAGCCCTTA GCATCAA	AAGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCCTACCGTGTGAGGTGGCCATGAAGCCCAAGCCCATGGAGAGACATTTTCAGA TAATCCCAGCCCTTAGCATAA[C/G]TCATCTTCAGTCTTTGAGTCTCTCCAGCCAGGTCCAAAGCTT GTGGACCAAGACAAGCC
WI-18012g	117	A G ---		---	TTTTATCTGGGTCAAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTC[G/A]TGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G A ---		---	TTTTATCTGGGTCAAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTC[G/A]TGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C T C C C T T	GCCACTTTTGC CCCTT	TCAGCGTGAT CAGGAAACA	TTTTATCTGGGTCAAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTC[G/A]TGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T C ---		---	TTTTATCTGGGTCAAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAAAG AGATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTC[G/A]TGAAGTGTTCCTGATACA GCTGACGTTTCGAGGG
EST38390 4	75	A G C T C T G C A T T G	GCAAAAAGGA GCTCTGCATTG	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGACTACACACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTGTA[G/A]TTAAGTTTATTAAATCAGCTGACTTTAGCATTTGGAGATTATCTGGAT

EST38512 7	91 T	TGACGATGCC AATACTTCG	CACTGCACTCT GGGAAGC	TAATAAAACTGACCCCAATTGGTAAACTGTGCTGGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACCTCGT/GGCTTCCAGAGTGCAGTGATAACTGTTATAGCC
EST38519 0	24 C T T	CCTGCACTCC TAAAAGATCT	TCTGTTAGGAC TTGGGGA	CCTGCACTCCATAAAGATCTTTTCTTCCCAAGTCCTAACAGAATGGTATATCTCTCGAAAAA AGATGAACGTCATCAATGGAATGTGCTGCTCTGCTTTGAGCTTTGTTTTTGTCTTGAGAACCTTG TCCTCCCTGCTGATTT
EST38575 1	66 T C A A	GAACATCCCA TGTTCTGTTT	AGGGAAGGTA GTATAACACAT	AGTGGTCAAAATGTAATACTAATGGGACACCAAGCCTCAGGAAGAACAATCCCATGTTTCTGTTTAA T/CJTCTCTTATGTGTATACACTACCTTCCCTTTCTTCTTTATACACATAGATTTCCCTTAATTGCAGC CCA
EST38616 9	101 C G C T T C	CCTGCTCCGCC CTTC	GAGGAATGGAT GGTGGC	CCATCTAGGCAAGCTACCTGAGCTCTCTGTGCTCCAGAGTGGTGCCTACGCCGGGGCCCCGTGG AGTCTCCGGGGCCCCGCCCTGCTCCGCCCTTCTC/GGCCACCATCCATTCTCCAGGGG
EST38652 8	59 T C C A T T T C A A	TCTGAACCTGGG C A T T T C A A	TTGCAAAAATG AAAGGAAAAA	TATAGTAGGTACTTTCCTTGTCTGCAGCAGGAATATTACGTCTGAACTGGGCATTTCAA/T/CJGCGTG GTATTTTTTCCCTTTCATTTTGCAAGTAAAAAATCAT
EST38654 5	42 T C G T T T T A C A	AATGGTCAATTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTTACATA/T/CJAGATAGAAGATTAAAGGACCAT CACTGAGGTACATAGCTCAGAGGCAGAGTTAAGATTGGACCCAGGAGTTGGTTCAGCATATA
EST38707 9	75 A G ---		ATC	GGATCCTCACTACCTGGGACAGCCTGAGAAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCCC/A/GJAGGCCAGCGGGATGTGTGCCCTCTCTCCCAACTCATCTTTTCAGGAACACGAGG ATCTTGCTTTCTGGAAA
EST38759 2	86 A G G T G A T A T G G	TGCTCCCTGA GGTGATATGG	TCACCATCGTG GACTTAAGG	TGACCTTGATTTCTCACTAGAGGGGAGAAGATCACCTACCTTTTGGATGCCTCCCACTCTACTTGT CTCCCTGAGGTGATAGG/A/GJCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAAAATCTTGCC TAGCAGCACC
EST38775 1	40 T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTCAAA	GACTCTCAACCAAGAGAAAAATCAATAGAGAGGATTGGCT/AJTTGAATTCAGAGCAAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCTCCAAATGCCCTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAAACCAACATGGTGG
EST38815 4	91 C A C A	TGTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTCACTTATGTGTGTTCAATCAACAAG TGTTATGAGAACCATTACACA/C/A/AAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38858 4	98 C T T G A C	CACGAGTAAA AAGAAACTCA	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACCTTTCCTCCAGTTTGGGGTGTTCATATTTGTTATTGTTATTATTA TTCAACACGAGTAAAAAGAACTCATGAC/C/TJTTCTCCTTGGACTCGCTCCTCTCCCCCAATCTCGAT ACCGACTGCACTGTTG
EST38865 2	72 T C T G T G T G A T G C	GCTGTAGAATT TGTGCTAGTTAA	GGAAGGACGG AGGACACAG	CCTTAATGGATTTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTCG ATGCT/CJCTGTGCTCCTCCGCTTCCCCAAATGAGCACATATGAGGGCAGGCAAGAGCATGCTGGA TTTGCTTAGTTGTTAA

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCCT CA	CCAAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAAAT/CITGAGGACATGAGATTT ATTGAAGGGGAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAACATTCCTCC TTATTCATGTCATCTCACACATTTCTTTATTTTATTTGTTTACATTTCTCAAAATATCGGATTTGTC TCATGAGAATAATGGCTGAGGGAGCTGGCAGGCAGTCTTCTCA/GC/GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	---	---	TTATTCATGTCATCTCACACATTTCTTTATTTTATTTTATTTTATTTTACATTTCTCAAAATATCGGATTTG TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGGCAGTCTTCTCAGGCTCCTCGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTCCTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	TTATTCATGTCATCTCACACATTTCTTTATTTTATTTTATTTTACATTTCTCAAAATATCGGATTTG TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGGCAGTCTTCTCAGGCTCCTCGATAGCTAAAT TA
EST38909 5	47 A G	GCACAGCATG GCTAAAACG	GGTATTTGTG ATTCCCATCTT T	GCACATAACTAATCTTTCATTTGTGGATTGCACAGCATGGCTAAAACG/A/GTTAAAGATGGGAATCAA CAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT AACTGAATGGCAGTGAAACACTACACATCAAACTTAGGAAATGTGGTTAGTGTGACGTTGAG GGAACTTTATAACCTCAC/A/GC/GCTTTTTCACAAAACACAGCAGACACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38911 9	85 A G	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTTGT GAAACAAGCG	TAAACATTCCTTGAATCCCTTTGGTGGG/GC/GGGGGGGGGTGGATTGAGATTCAGTGTCAAGATAAA TATCACAATAATATCAAAAACCTTCAAATTTGTCTATGCTATGCATTCACACACTGACATGAGCCACAACAT CCTTCACAGGGACTGTAC
EST38955 5	30 G C	TGAATTCCTT GGTGG	CACGTGCAATCT CACCCC	CCTGCTATGATGCCTGGGAGATCCCGGACCTTCGGTGAC/G/A/CAGGCTCCCTGCCAGGGCTTGG CCCCTGACCGGGCTCCCCAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39002 0	42 G A	GGACCTTCGG TGACC	CTGGCAGGGAG CTG	CACGTGGCCCTAAGTTTCCGGTCTTCTCAGTCTGGATGGCTGTGGAAAAGCTTGGTGGTAAG GCCTAAGGAATTTGAGGGGCAAGGGGCGATGCCCGCAGCCGAGATGGTCTGTAAAGCCTGTGGGTC AAAGACCTAACTTCTGGA
EST39004 8	79 T G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGC	AAAGATAATGTGCATCACACGCAACATATAGAAACATAAAAAGAAAAATAAGTATCCACCCTAAAT CCCTATTATTCCATGATATTTTCA/T/C/JAGCAACTAGTATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16398	90 T C	TCCCTATTATT CCATGATATTT TCA	GAATGGTTGT GAAAAATATA TTGATAT	GGTTGCTTTTCATGATTTTCTCATTTCTCATCAGGTTTCTGGTCTTTTGTCTCAATTTTAAACACTT T/C/CTTTTATATAGGGAATAGCCCTTAACTGTGGTACATGCTGCCAAAATTTCTCCCGATT
WI-16403	69 T C	ACT	AAAG	GCTTTAATGGC TACAGAAAGA AGG
WI-16406	24 C T	AGG	AA	GCTTTAATGGCTACAGAAAGAGG/C/TGGTTTTATTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTGCAITTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G G T C T	TCATCTGAGA ATAAACTTCCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTCATGATTGTTTCATCTGAGAATAAACTCCTGTCTAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63 G T G G A T G C C	CCTGAAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAACAGGGATGCC[G/T] TTCTCGTACTATGTTTAAATGTGCTGAGCCAGCAACCCTCGAGTTACCCGGCCTTTTACCCCCAGCC AGCTGCTGCTGCTGCAT
EST39366 2	72 T C ---	---	---	AGAAACATTCGTCTGATCAGAGGAAGATGTATGTAGAAAATCAGAATCTGACTGAATTCTCTAAA ATCTATT[C]ACACTGAGAGGAAAATGAAAAAGAAAATGTTTGCAATAAGCTTTTCCCTGACTCTCA GAGGGGTTGAGA
EST39371 9	86 A G C G T G A G A G G	CATTGGATTA GCGTGAGAGG	TGATTTGAGAC ATTTACATTT TT	AAAAAGCTGAGCTGGCAAGTCAAGTTTATTTATGTGTAAATCCCAGTTGAGCATTTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAAATCAAATGCTTCTCTAAAGATTA GACATTGCCCAACCCCTGC
WI-17177	23 A G ---	---	---	ACAAAGTACATATCCAAACCAACC[A/G]TCCATCCCCACCTGTGGCCCTATTCTTCTGTTCTTT AGAGCCTTTTCAGCTATTCTCTGTGAAGCAAACTGCACGAAGGCCTCCCCGTACTCTCCCTGGAA G
EST39428 8	31 C T A T T T G A T T	GCTCCCCACA ATTTTGATT	GGTCCCTTATG AAGCCACC	AGGTTCTGGTTGCTCCCAAAATTTTGATT[C/T]GGTGGCTTCAAGGGACCCAGGATTCTGCATT TTCTGGTGGGCTAGGTAATCTGTGCTTTGGTCCACAGAGCACAAATTAAGAGATCAGGTCT GGCTGTGC
EST39430 2	45 A C C	GGCAGAGGAA TAACTGATGTT	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/A]CAATACCCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGGAGGATGTCCTGGG
EST39446 7b	117 C T G A G T A A	CTACTGACAT AGGGACTTCA	TCCTGGAAAAC TGACATAAACC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAGAAAATAACAGGAACCTATTTATAT ACGTAATACATTTTCATACCTGCCTACTGACATAGGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTCCAGGATTGTTCTCC
EST39465 2	80 A G G T G C C	AATGCAGGAG GGTGGC	CAATCTCGGCC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAAACGAACCTGAACAGAAA TGCAGGAGGTGGC[A/G]AGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G A A C A T T A G	AAAGATTCTCT GTAGACATCT	CACATTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTTCAGACATCTTGACCAGCCTAAAGATTCCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATGCAAGTGCAAGTTCAAGTCAAAACCAATTC
WI-18387b	84 A C ---	---	---	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGTGTC CATGCTTTAGCCATAC[A/C]CATGTTGAACATTGACTATGGAGTCTTGTAAGAGTGTAAATGTGCGATG GCTATGTAGACATAAGA

WI-18387a	57	A	G	CC	CTTACTTTGG	GCTAAAGCATG	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGAACCCCATACAC[CTTTTG
EST40601					CGTACCCCAT	TGACCACAAA	GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGCTTTGTGAAAGTGAATGTGGGATG
9	78	A	G	GA	CGTGGAACCT	TTCTTGAAGA	GCTATGTAGACATAAAGA
					GAAACAC	AAGCGTC	TCCAGGATGGTTTATCCAAAGCTGTGGACGGTGAACATTAAAGACAAAGAGGTGACTCGCGTGGA
					AGGTATCAC		ACCTGAACAC[AGGACGCCCTTTCTCCAAAGAAGGGCTGTGGCGATTGAGGCACTCAAGG
EST41935	32	A	G	AG	ATCTTCAGGAT	GCACACCCTTC	TCCATTGAGTGTATCACATCTTCAGGATAGGT[AGTAAACAGTGAAGGGTGTGCTCATTTCTTC
					AGGT	ACACTGTTA	AGCTGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTTGTGA
EST43091	28	C	T	CA	CATTCTGGTCT	AAACTGATTT	ATGTCATTCTGGTCTTTATTTTGGACA[CTGTAGCATGTTTAAACAAATCAGTTTTCATAGGCAA
					TTATTTTGGAT	GTAAACATG	CCTTTGAACATCAAAAGAAATACAATATATTTTCAAAATTTCTCATCTACTGTAAATCA
WI-18420c	108	T	C	C	TTCCATTAAAC	AAATTCAGC	AGAGAGACAACAAGAGAAATAGGAAATGGGAAATGGGAAAG[CTJAGAGTGAAATTAAGCAAAATCTT
					AGGAAGTTT	ATTGCTATAAG	TTCCAGATTCCATTAAACAGGAGTTTCTCATAAAATCAAAAT[CTJGCTTATAGCAATGCTGAGAA
					GAATAAGGA	C	TTTCATAGGTACTTTCATGGGA
WI-18420a	38	C	T	AA	GAATAAGGA	CCAAGATTGC	AGAGAGACAACAAGAGAAATAGGAAATGGGAAAG[CTJAGAGTGAAATTAAGCAAAATCTT
					AAATGGGAAG	TTTAATTTAC	GGATTGAGATTCCATTAAACAGGAGTTTCTCATAAAATCAAAATCAATGCTTATAGCAATGCTGAGAA
					AA	TC	TTTCATAGGTACTTTCATGGGA
WI-18425b	101	T	C	---		---	AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCCTGTC
					CACCTGTCT		CTAGACAGATTCA[CTJGCACACAACACAGGAGG[CTJGGGGGTACACGGCGGAGAGGCCAAAGAC
					AGACAGATT		TAGGGC
WI-18425	81	A	C	A			AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCCTGTC
					CTTTTGGCTCT	CCTCCTGTTGT	CTAGACAGATTCA[CTJGCACACAACACAGGAGGTTGGGGTCAACGGCGGAGAGGCCAAAGAC
WI-18449	129	C	T	A	AAGTGGGACT	TGTGTGCA	TAGGGC
							AAATTGAGGTCCGGGTGGAACATAAAAGGAAAGGAAAGAGAGTAATCAAGGGAGGCCAAAGTG
							GGAAGCTGATTGCTGATCTAACGTGCTGTTCCAGTTCTTTTGGCTCTAAGTGGGACTA[CTJTC
							TGGATACAGTCAGGGGAG
WI-18457	120	T	C	---		---	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCACTGGTGGCCCCCAAGACATTATTTTATTCTT
							AAATGTCCAATATCTGCCTGATGCTGTGTTTGTGCACATTGGGGCCACAG[CTJAAATAGGCTAAA
							AGGAGTCCACCTGCT
WI-18462	39	A	G	AG	CCACAATGGC	TTTAGGCTTTG	GGTGTATAGCTGCTTGTACACCACATGGCAGAGGTGA[GTJAGAAACCATCTCAAGCCCTAAA
					AGAGGTGA	AGATGGTTCT	TATTTACCATTACATCCCTCACAGCAAAAGTTTGCTATCTCGGGTTTAGGACTCCATTGAG
WI-18476	60	C	T	GAGG	GGTGGGGTGC	GCACGATGGGA	TGAGGAGGTGTACAAGCTCCAGCAGGGGTGGGGCCGGGCTGAGGGTGGGGTGCAGGG[CTJGGT
						GTGACC	CACCTCCATCGTGGCCCTGGCCCTCCCTCCACTACCCACACCTGGCCACGTTGAGGT

WI-18491	109	G A	AACAAATGGT AGGTGGTATT	CGTGTGCATT TCITGTAATCC	CTAATGAGATGAATACATGAAGGGCGTTTAGCACAGTGCCTAAACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAATACTATTATTATTAATCCAGAAATGAC[G/A]GGATTACAAGAAATGCACA OGT
EST50757 b	79	C T	GAGCTGAGG CTGCTTCT	ACCCTTCACCC GGCC	AGCCCCCTCCACTCCACTCTGCTCCACAAAGTCGGCTCCCGAGAGCTCGAGGCTGCTCTCTTTTATAT GTGACGGCC[C/T]GGCGGGTGAAGGGTCAGAGA
WI-17675	103	T C	GGACATTTGG CATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGGAAAGCACTAGAACTAAACATCTTACCAGGTGCTGAAGAAAAGTGTCTTCGTTTTAAT TGCCAAAGCAGGGATGTGGACATTTGGATGGTACTT[C]CCTGGGTGGTTCCTCCCATAGATTCAACCAT TGCCCTCTAATGGTGCTA
WI-16543	67	G T	AGATAAACTA CATTTGGGTTT	GATTCATCAT ACAGGGACTT	GATCCATTACCTAGGTAAATTTCTCCTGAATGTCAAACAAAGAGATAAACTACATTTGGGTTTTGG G/TAAAGTCCCTGTATGATGAATCAAGAAATCCTCAAGTCTGCTTGCCACCCATTTAATACGTATT TTTGTAAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAAGG TTGGGGAA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAAACCATCTCCCCCTGACCCCCAGTCCATGGAAAAATTTGTC TTCCACAAAACCGGTCCCTGGTGCCAAAAAGGTTGGGGA[C/G]TGCTGGTGGGTACAAAAAGTAATT G
WI-17690b	79	A G	AGGCAATTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAGATATGTTGCTTTACTACAGTGGAGGCAATTTTCTAGCTGTGTTTGATT GGCTTCCCTAT[G/G]GATTGAGGACCCATAACTCTTGTTCACATCATCTGCTATGCTG
WI-17690a	63	G A	AGGCAATTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAGATATGTTGCTTTACTACAGTGGAGGCAATTTTCTAGCTGTGTTT[G/A] TTTGGCTTCCCTATAGATTGAGGACCCATAACTCTTGTCTCCTCATCTGCTATGCTGCTG
EST51717 b	128	C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAAATCTCAGTGTCTAACTCATCCTCCAGATTAT[C/T]TGAAGTGGAACCCCTCCGACCC TGGAACATCACCCTACCTGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGT[C/T]GAG CTGGATTATTGCCTCAA
EST51717 a	39	C T	---	---	GATCCAAATCTCAGTGTCTAACTCATCCTCCAGATTAT[C/T]TGAAGTGGAACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCTCAA
EST53012	97	C T	TGGTCACTTTG GGGC	GGCTCTGCCCA GGC	TTTCCAGGTTGACAGGTTTATTCCACCCCTTCCATCCCATCCCGAGGAGGAGGAGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCC[C/T]GGCGTGGCAGAGCCCACTGGGTTTACATTCTGT GGGCAGGTGTGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTACAT TT	AACTGCAATAACAAAAACAGAAAGTCCAAAGAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACAATGTAC[G/A]AAATGTGACAAGATATCCAGATGTTAA
EST53389	74	A/G	GGAGACCTGC AGAACTTAA	GGCCTTTCTAA CAATAAATGCT C	TTTCGAAATGTCCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT TAAACAC[G/G]GAGCATTTATTGTTAGAAAGGGCAAGCTTTACACTCAATAGGTTTTAACATGAAC ACATTAAAGGGAGATGGCC





[illegible]

TIGR- A003P30	117 C G ---			ACAAAGTTCAAAGGAGAACTTCCTTTGTTTAAATGCAGCTGTGCTCAGAAGCCCTGTGATTTCTCCTAGGA AACCATCTGGGTTTAGCCCATAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TIGR- A004S34	156 C T A	CCAAACCTCCT CATTCCATATA	TTAAA	GCTTGCTTTTATGTTAGGTTCCGGGAAAGAAAGGGCTGACAACCCGAGACATCTGGACACCAGC AAGGGTCCAGGGGAGGTTTGAGAACTTCTTTGCTTGGCTAACAGTCTGCTATGTGACAAATAGCCA AACCTCCTCATTCCTATATAA[C/T]CTTTAACAAAAACAGTAGCTGTTTACAAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97 A C ---		---	AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCCAAAAATGAT TGAGTATGATAAAGAAATTTGCATGGCGATT[C/G]AAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAGAAACAATATGACTTAGCAAAGAAACAATATAG
TIGR- A004T44a	69 G A TGA	GGAAGATAAA CCAAAATGAT	GCCATGCAAAA TTCCTTATCA	AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCCAAAAATGAT TGA[G/A]TATGATAAAGAAATTTGCATGGCGATTAAATAAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAGAAACAATATGACTTAGCAAAGAAACAATATAG
TIGR- A004V08	60 T C GGCATTCTCT	CAGGAAAAACA	TCCTTCCCACA AAAGGC	CCTACAATCCTATAATTTGCAAGGGTTGGGAAGGATGCAGGAACAGGCATTCTCTTAT[C/G]GCC TTTTGTGGGAAGGATCAATTTGGTGATGCACCTTAGGGGACAATTTGGGCAGTAGCTGTCAAAATTC AGTAGCTGTCAAATTTCAAA
TIGR- A004V26	125 A G ---		---	TCTAGCTATAAGACCAGATTTAAATTTCTAGATATAGAAATATCCAGAAATAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA[A/G]AAGGT TTCAGTTTATAAATGCTTAAATCTGTATCTAATTTGCTTAAATCTGTATCTATTGG
TIGR- A004V28 a	29 A G CGATCTC	TGTTGTGGTG	CGGAGGTTGCA GTGAGC	CCAGGCTATAATGTTGTGGTGCGATCT[C/G]GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCAOCCGCCACCGCACTAACTAATTTTGG TATTTTATAGTAGAGACATTGTAATTTTATAGTAGACAGG
TIGR- A004X20	25 T C GA	AAGTTTTCCCT CTCTTCTGTAG	TTTTATAGTTG ACTGTAACATG GAGAC	TAAGTTTCTCTCTCTCTGTAGGAT[C/G]GTCTCCATGTTACAGTCAACTATAAACACATGGCTCATGT TCACTCTGGGCTTCGCTCAGAGGAGTTTGATATTTTGGAAAGTGGTACCTTTGTTCTGTGCTTTTCA GACCAACCGCTCTTTCATTTCTTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCTCT
TIGR- A004X30	26 T C CCAC	TTTGAATCTT AGAGTAGAAC	TTCTTTATGGA AGTGTTTAAAA CTATTTT	TTTTGAAATCTTAGAGTAGAACCCAC[C/G]ACTCTAGTAATACTTGTAATAAAATAAATAGTTTT AAACACTTCCATAAAGAAATAGGGTGCCACAGCTCCTTGATTTCCCCCTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102 T G ATGCAAAACT	TTCATTTGGGT	CTTATAATTAG AAATTCATGA AAGCAA	CACGGTATATGCCTTATATATAGGTATATATACAGATCGTACACAATATAATTAACAGTTTGACATG GGGTCCACAGTACCTTCAATTTGGGTATGCAAAACT[C/G]TTGCTTTTCATGAAATTTCTAATTATAAGG ACTGTTGCTTCTTCATATATCAATGGACATTATACAAAAATACAGTCTCTTTAGTGAATTAAGACGTC TCTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C T	GAGAACAACT GCAGCAATTTT	AAGATGGTGCAT CGGGAAGA	TAAGTGGAGACAAGTTTATTGGAGGAGCTTGACACCCCTCTTCTGCGCTAGCTTGAGAGAACAACTGC AGCATTTTTTCTTTTTC/TTCTCCGATGACCATCTTTTGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAAGGAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGCTGCGG GTCC	GTCTAGCAGAGGAGATACTTTGAGGGACAGCCCCAAGGGCCAGGTAGCCTTCAGGGGGCGGCA GGGTTGGGGAGGTAGGAGACTCTGGACCGGAGCGCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TIGR- A005D17 c	81 T C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGC/CTGTAGATCTCTTGGCCTCTCTGTGCGAGGATTCCTTCTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TIGR- A005D17 b	79 G C	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAG/GC/CTGTCTAGATCTCTTGGCCTCTCTGTGCGAGGATTCCTTCTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TIGR- A005D44	97 G T	TTAACATTATT GAACTTAAAA CTGTATACAC	TTGTCTATTAT TTAAAGCCAA AAAA	CATCAGTAACATATACACAATTGGTCACTCAACTGAACCTTGGCTCCAATATATTTCTATACAATACTT AACATTATTGAACCTTAAACTGTACACTG/TTTGTGGCTTTAAATAATAGACAATGATTTTG TCTATTACTTAGTATAGACAAGGTGATTACTTTGTAGACAAGGTGATTACTTTGTTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAATTTATAACCAAGGCTCTG/A/CTCACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTGGCTGCTTGGCCCTACAAAGCCACTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	---	---	CTCAGTGTAACAACTTTGTTTAGGGAAAAAATAATCCAAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTGTGAGACAGAATGACCCCTGGGCTCCTTTATTTGTTCTTTTCAACAGGACC CCACAGATAATTTGCGGTATGTCATGAGGACTGGGATGCTTCTATTG/C/GGATGCTTCTATTTT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTTGTATCTTAGTAAGGTACTGCACCTTACAGAG/A/G/CTCAATTTCCCTGATTAGGA AGCGATGCTAATGGGTATTGCATAGGTGTAAGTATAAAATGTTGTTATTAAGAGAATCCCAAG CTTGGTATAAGGCAGAAAAATAAATGGTATAAGGCAGAAAAATAAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGTAAAGCACCTACTGCGTATCAGGCACCTGACTCGG TGCTTTAC/A/G/TACATTACCTCACAGCCAGGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/CT/GCTTAGGGTGTCTCCCCACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGCACTTTGTCTGCTTACGAGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTCTCTTGTATATTTGTAAAAATTTCCCAAGAGCCGCGCATATGATGAATCTGCC

X57830	106 G C C T	AGTGGAAACA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGGAAGTTTTCACCTATCTCGAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAACGATCATATCTGTCATATGCCTCATTTTATCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGTGCTTGAAAAATGTTCTGACAGCATTTACAGCTGTGAG CTTTC
X74070b	72 T G T G G A T C	CTTTTAAAGAA ATTTTGTTTA TGGATC	GGGCTTAAAAA TATTAGAGATC TAGATT	AACCTGAAGAAGTTACTGGAGCTGCTATTTTATATTATGACTGCTTTTAAAGAAATTTTGTATTG GATCTT/GIGATAAAATCTAGATCTCTAATATTTTAAAGCCCAAGCCCTTGGACACTGCAGCTCTTTT CAGTTTTTGTCTTATACACAATTCATCTTTCAGCTAATTAAGCCGAAGAAGCTGGGAATCAAGTTT GAA
Z48804	44 C T ---		---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGTCTCATCACAGTC/TTAGAGCTTCTTCCCGAAGGG CCTTTAGGATAGGAGAAAGGGTTCATGCACACACGCTGTGAGATGGAAGAGCCCCCTCCAGACCACT CTACAGCTGCTTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAGTAAGTGTAAAG TCCA
D28513b	133 A G ---		---	ATGACCAAAGCCACCACATTTAGAACTTTGGCTGCCTTTGGAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACCTTTGGACATGGCTCACAAGCAGTTTGTGATTGACTGCATGAATGC/A GTTGCGGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACAGTTCTGTCTTC AGCTGTACATA
D29833b	85 A G ---		---	CCACTCCATCTGATGCCCCAAGTTATCCACAGCTCTTCCCGACCAAGACCTATCCACCTGGACC TCCATTTTCCCTGTAA/A/GTTCTCCAACTGATCCTACCCTCCCTACTCTCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCAACCAACCAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21 A G ---		---	CCACTCCATCTGATGCCCCA/A/GJTTATCCACAGCTCTTCCCGACCAAGACCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTCCTCAACTGATCTACCTCCCTACTCTCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCAACCAACCAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D31762	82 G A ---		---	CTCCCTGCCTCCTCCTCTGCTGCTGATGCTCGTCTCAACAGCGCAACCTGTCTTGAATGGGG GAGGGGCGGTTT/G/A/JCTTCTCTCTTCTGCTTCTCTTATCTTCCACAAACCATTCCTCAATAAA GCCAAAATCTTCTCTTCTCTCCCTCAGGCCACCTCTGTCTCACTCTCTGCTGTGCTGCTTTT CTGGA
D37931	64 T C ---		---	ATTATCGGAGTGGTTGACCTTACACTTACTCTCTTAAATAGCAGTGAGTAATGCAATTTGAGCTG/J/C CCCAGGCTGTCTCCTCAGCTCATTTCTACTCTTTTCTCTATATAACTCATTTATTAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAAATGAGGCTGGGCTTTTCTGTAAATAAGCTTCC TTT

D63807	101	CT	---			CAGGAGGACTTCAGTGTGATCCCTGCCCTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGTGTATTTTCTGTTCCA/C/TJGAAGAGGACTTTTGTTCACAAATGGATCAC AATGCAGAGGAGTGTCTCCTCCCGCTGGCTCTCGGTGCTGGGAGGTGACCTGTCCAGATGAC TGGAAACATGCGTGTGACCTC/TJACAGCTACCTCTTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGGGACTCTTCTTAACITTAATTTAAITTTATTTATTAATACTATTAGTTTTTATAATTTATTTTGAT TTCACAGTGTGTTGTGATTGTTGCTCTGAGAGTTCOCCTGTCCCTTCCCTCOCCTCACAGTGTG TCTGGTG
D90145	21	TC	---			ATTATCACTCTCAAAAATTTGGTGTGTGTTTAAAGTACTTTCTTATTTATGAGCCCC/TJ/CJGAGGA CCAGACATGTTATTAACAGCCCCCTATATACCATCTAAT
EST14035 1a	59	TC	---			GCATTTTAAATTCACATTGAATCATTAATTTACTATTTATGATGTTTACATAACAATTCAGTATCATTT ATG/C/TJGTAGATTCAGATGTAGGTGCTCAATACAGCACCTTATCT
EST16668 5	71	CT	---			ACAGACTATCGCCAACTTATAATGCTTAACTTTATGATCAATAGTAATAAATTACA/C/TJGAGATA TTCACACTTTATTATAAATAGGGTTGTGTAAGATGATTTTCCCAACTGTAGGTTAAACAT
EST16904 7	57	CT	---			TTTTAAGTACCAGAGGCTGCTGGAACAGGATGAAACTGATACACC/JG/JTGTACTACTTACTC TTCACCTTCAAACTGATCCCTAAAGACTTCTACTTAGCAA
EST21863 9	49	AG	---			GGCTGTAAGTAGAATCAAGGTTAAGAACATTTTATGCACTTATTCACAAACATTTACTGAGCATA CTAGGTGCTGGGAG/JTGTGACAGTGAGCAAAAACACAA
EST21885 6	80	GA	---			ATTTAGTGCAATGACAAAGCCCCAA/JG/JAGAACAGAGGATCAAAATAGATTGAAATGTATTACC TTCATAGTATACGAAGTTTAAACACAAGTATGGGAGT
EST22623 8a	26	AG	---			AAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTTATACAG/JG/JAAATGTGGAAGAGATGGCTTTTAAACCCC
EST22644 2	98	AG	---			CCTCATTTTAAAAGACGGACATAAAAAT/JATATACAAACAAAACCCCAAGTCACATTTTCAG GAGGTAAACCTAAAAAGTCTGATATGAAAATATGGTGG
EST23587 1	31	TA	---			AAAGATCTGGCATTATTCACATCATTTCTAAATATTTTGTAAATTTTCCATGAGTATTTTTTCA TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACC/TJ/CJGAATAACCCATAGTTACAGAAATGG GTCTGTGAACCTCAAT
EST24246 7	106	TC	---			TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/JG/JCATTTAAAAATGTATCAAT GCACCTTCTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24308 3	45	AG	---			CTTGAACCTCTGGTCTCAAGTGGTACGTCGCTCAACCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC/GA/JTGCCTGACCCACATTTCTTATCCGATCTGTGATGGACATTCAGGTTGTTTC
EST24435 6	73	GA	---			TATTGTTGCATTATCAAAATGGTTA/TJ/CJAGTTTTCAATTAACCTGTAATTTGATTTCTATGTATAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAATCGTTAGTTAATGCTACATT
EST25089 6	25	TC	---			

EST25476 9	33 G A ---			AATGATCTTTATTTCAGACCTGCTCCTAAAA[G/A]CTTCTCCTCCTAAACCAACCAACA AGAGGTCTCTTGCTGCCTTCCATGGACTGTGGCGGCTGTGGACTTGGACCGTCTGCTGA
EST26183 2	70 T A ---			AGATAATGCATTAGAGCCCTCATTTGATCTTGATTAACCTTTGTAAAGATTGATCTCTAAATAAG ATT[A]ACATCTCGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 T C ---			AGAAAATAAGGTGCTACCAGAACTCATG[T/C]GATAGCGCTTCTTTAGGCACATATTATAGCAATT CAGATGAAAGTTCTGTAAATCACACACACACTGTGCCCTCTAACAAACACACGGTGACTCTGA
EST27816 5a	26 T C ---			CAACTCAAGGTACAAGACAAATTGCAT[T/C]TAACATTTTATAAATAAAGGAACATCAGATCAAT CATTAAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST28588 0	78 A T ---			GTTTAATTGGCGTATGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGAGGTCTCAGGAA ACTTACAATCA[A/T]GGTAGAAGGCAAAGAGAGCAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST30226 5	25 A C ---			TACTCACACCGACATACATATCTCA[A/C]GTAGAATTAGCTATACTGCATACTAACTTCATTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGCTAACTTAAACAAGACAGACTCATTTCCTTTGA G
EST30935 9a	59 C G ---			AGCTATGGTAGAGCAAAATCCAGTGGTGGTAAATCAAGAACTCTAAAGTTTCAGTAGAGA[C/G]AGGT GTTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25 G A ---			CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCCTCTAAAACCTGTGTAATAGAATAATGGCCAAT ATTACAGTTTCTCATTCCATGAACTACTGGCAGTGTATTTCATGTTTATATGTGAGTTTCTATGC ATAAAATCCCAGTAAGA
EST33274 4	27 T C ---			TGCTTTGTTCCCTCCAAATCTCTAAAAT[C/G]GTGTGCTTCAAAGAAATTCGTGGAAAGGACTTTGAA TACGAGTTTGACCATATTCAAGTATTCTTGAATACAGGTTTCAGATACTATGGAGATGATACCAATT GGACTAGGTA
EST33352 7b	75 C G ---			TACACATTATCAAGAGACCACCTGCATGCTCTCCCGCAGAAATACATTCGTCCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTATTTACTAAGAGAAATATCTCTTGGTGTATATCTAGGGG
EST33424 1	126 A C ---			ATTTTCCCACAGCAGAGTATATTTATGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTGG GAACCAGTACAGAAATGTTTCACAAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAA CAAAGGTGTTGAATCCTCTT
EST33488 7	90 A G ---			CCTTTGGGGGAGTTTAAAGCCAGAATGTGACAAAGTCACTTACAGGAAGACTGGAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]ACCATTTCCTCCGCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b	45 C T ---			AAAAACATGCTATTTGAACAAACTTTTTTATAAGAATAAGTTGA[C/T]TGAAAAGCAGTTTTTAAAT AACATCAACTCACAATGACTTTTTAGAGGCCAAATAA

EST33508 1a	36 A G ---			AAAAACATGCTATTGAACAAACCTTTTATAAAGA/GJTAAGTTGACTGAAAAGCAGTTTTAAAT AACATCAACTCACAATGACITTTAGAAGCCAAATAA
EST33863 4	77 C T ---			ACAACATAGGACTGGTATTCTTGGTTTGA AAAATTATGTTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAAC/C/JTCTTTGAACACAGCCTGAATCCCCC
EST34739 3	97 T A ---			GAAGTATCCTTCCCAGTGGCAGGAACCTGAAGACTCCAGACTCAACAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGGAACCTC/T/AJGGTGCCCTTACAACCTCCAACACTACTGCAGAAATTTCT TGTTGTCCTCATAAACA
EST34792 6b	104 A G ---			ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCAGACAGATCACGTGGCATCCACTATCAATA CTCATAAGCTAATTTATCCTCAGGATGTTCCCTGA/A/GJGATTCAAGGAATCTTAGTCCTATTACA AAGATTTGTTGCTGTG
EST34835 9b	93 T G ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGCTTTCTGGT/GJGGCCTTAAAGAAACAGACAAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTG/AJTGCTTTCTGGTGGCCTTAAAGAAACAGACAAAATTTGTGCTAAAGAT
EST35230 0	93 G T ---			CACAAAGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAGAGGTTCTC/G/JGSCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---			TCITTTCAAATTTTGTAGGCATTTAATG/C/JJATAAAATTCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTTGGGCATGTTGTGTTCCATTTTACTTAGTTCAGAACITTTTCAATTTTCATCT
EST35708 9	32 C T ---			CTGCCCCAAATTAACTTTAGGCAATGGAAC/C/JAGACTTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGACGCGTGTGCTTCCCTCTCTGAGGTTGGACCTTTTCCTGTTGTG ATGTGCAAGTGTGGCT
EST35747 9	51 C G ---			ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCCAAAAGGCTCC/C/JATGTTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---			TGGTCCATTATTTAAACCTGAGGGAACAACCGGTGCTGACATGGCAGACATTTATTTCAATGGAGA AGTTCCCTCCCATGAACCAAGA/C/AJCTTGCTCCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATAATAATTAAGCCTGTGA
EST36301 4	93 C T ---			CACCTGTTCAATTTGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGCCTACGCCTACAGC AGTCAGGAGGCGAGCCATGGCCCTG/C/JGCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T ---			GCCATCAGCCCCACAAAAGACATGACTACCAACGC/G/JGGCCCCCTTGCAACCATACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGCTCTAGTCGT

EST36620 6	50	G A	---			GACITTTATAGATAAGGGTTTCGGCTACCCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTTAAATATGGGAAATAAAATACAAAAGGGCCACACCCGATGCAAAAAGACTTT
EST36690 0a	89	C G	---			CCGTGATGTGCATGGTGCCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCAGCTATGTCAGGA AAGGAAGTCTGGGATTCCTA[C/G]AGGGGACATATCACACATATCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTTCA
EST36729 9	62	C T	---			GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCCTCCTCCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACCTTTAGCTACCCCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103	A T	---			ACTGCTGGCCGATGATTGGAGCTTGAAAAAAACTTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATT[AT]TCTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126	C G	---			ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88	T C	---			GGTCTCACTCTCTTGGCCAGGACGGTTTGAACCTCCTGAGCTCAAGTGACCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACACACCTGGTCTTGTTTAAAGTAACCACTGAA C
EST37269 3b	105	T G	---			AATAGTCTATGGTACGGCCCGTGGGATGTTAAAAATTGGGATTTTAAATTAAAGATTGTGAACATG CAAAACAGCAAAATTTCTCAGCTTATATTTTGAAGTCT[T/G]CAGGAGAAAAAATGGGTCC
EST37284 2	93	G T	---			AAAAACCTTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAAGAA GCTCTCGGATAATGTCACTCTAGGAA[G/T]AGTAAACAGGTGTTAAAAACCTGAGATAGCAACCCCT CTTGGCTTCTTGAGGAATA
EST37315 2a	90	A G	---			AGATGGGGTCTTGCTAGCTTGCTCGGGCTGAACCTAAAGATATCCTCCTCAGCCTCCAGGTAGT TGGAACCTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACCTTCAAGTTTGTATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45	C T	---			CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACCTT[C/T]AAGGGTGAAAAAGCATACC ATTCCATTTTAGTTGAAATATTCCTTCACATAGCCCAACACATTTTTCAGGCACTCTAGCTACTACA CGA
EST37376 8b	101	G C	---			GTGACATCATGTCCTTCAATGCCCTTTCAATTAAATAGTAGT[C/T]GAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCAGAGTGCTGTCTCTGCA[G/C]GCTGCTCCTCAGGCAAGTTGCTGACTTCTCTG TGTCAGG
EST37376 8a	41	T C	---			GTGACATCATGTCCTTCAATGCCCTTTCAATTAAATAGTAGT[C/T]GAGCGCTGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCAGAGTGCTGTCTCTGAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG



EST37378 9	63 T G ---			ACACACAAAAAATGGTGGCAGAAAAATCTGGAAAGATTCTTAATAACCTCAATTCGTGAAAACT/G JAACATGCCTCAAAAAAGAGGGGAAAAAATTTAAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A ---			AAGACATAAAATCTGCAATGAAATCAGTTATGAAATATTAAACCTCTG/AJCTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAATCATGACGTAGAA
EST37613 6	34 A G ---			CTAGGCATGGGGCTTTACAGTCATTTATTACCA/GIGTCATGAATTCATTAATAAACCCACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCCCAAAATCACCCCTGCGTTCATGGATCTTCCATCTAA
EST38025 4	56 T G ---			TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATATCACTTAT/GJTTATCTCA ACAATCTTGAAGGGTGTATTATTTCCCGTCTTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57 C T ---			TCTACCAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTTA/CJTCGCATGG AAGAACGCTCTCCTTTTAAATCCCTAACTCTCTTCTTCTGGGAAGACAGAACGTGCACAA
EST38420 6a	100 T C ---			TAAATCAAGGCCTCTTTCATTACCAAAACAAACAAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGCATCCTGACTGACT/CJGTCCCTGCAGTGCCTATGGGTCCCGTGCCT TATTCACTTCTCCTCTCA
EST38950 5	25 T C ---			TTTATTGCAAAAGTAAGCAGCCGGT/CJGTGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCTCG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90 T C ---			TTTTTTGTTACTCTGTAGCCAGTCATTAACTGAAGGTTTAAATATATCATTTTATTGGGATGAGATCA TAGCTTTACACAAATGCTATGTC/JAAACAAGTTACTGAATAATTTTACCCTCGTGGAGTTG
EST39331 1	70 G C ---			TCCTTCTGCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAGCCATGGAAGGAAAGTA TGCG/CJGTGTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31 C A ---			GTCAACATTGACCTTACATAGTGCCTCTAGT/CJACCTATGAGGCACCTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37 T C ---			TTCTAATAGCATGCCCCTGTGACAGGGAAACTAAGCTC/CJTCAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTTGTAGTTTCTCCAGAAGGCTCAAGGTGTTG AATAATCTGTGGGACTCA
EST40549 1	42 A G ---			TGTTTCTAGAGAACCTGTGTGATACACTACCGATGCACA/GJATAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACCACCATTTCTCACTTTGAACCTAGCTCCCTGCAAAGCACCTTCTA CCCTGCACCTTTGGGGAG
EST40579 1	81 A C ---			TGTGAATTACACATCAGTAAGCAGTTTACAGAATTTTACTTCTTACCTAAAGCTGTGCTATCTG AGCTGGTGGAAA/CJGGACTTGGAGACAGCGAATTTAAATACGGAACAAGGCTCTCCAGGAAG
EST40584 3	68 A G ---			TTGTATGTTGTAGGAATTTGGGAAGAAATATCTGTGAAGGAAATTTGCCACTGTAAATGCACACCC A/GJCTGTACTCCCCACAATATCCTATGTTTTAAGCT

EST51340	51 G A ---	---	---	GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C ---	---	---	CATGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAACATAGAACTCAGAGCCAGATCCTTTATCCAACICTCGA T/CJTTCCTTGGTCTCCAGTGAAGGGAAGCCCATGTATCTCAAGCAGGGAAGCCCCAGTGAGT AGCTG
K01506	63 T C ---	---	---	CTGAACCTCAGCTGCCCTACAAACTCCATCTCAGCTTTTCTCTCACTTCATGTGAAACTAC[T/C]C CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTTATCCATTACCTCAAAGCAGTCAITTCCT TAGTAAAGTTTCCAAACAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTC ATTGAGCCTTTTATCCT
L18877	69 T C ---	---	---	TGAGCTGAGCAGGAGTTGCAGCAGGGCCAGTGGAGGGAGTCTGGGCCAGTGCACCTTCCAAGGCC C/T/CJATCCATTAGTTCCACTGCCCTGTGTGACATGAGGCCCATCTTCACTCTTTGAAGAGAGCAG TCAGTATTGTAGTAGTGAGTTTCTGTCTATTGGATGACTTTGAGATTATCTTTGTTTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---	---	---	GCATTTTACATATCCCAAGCCCTTTAGGGCTACAG[T/C]CTCTGTCTCTGGACCCTGTAGGGTGCCA TTTGAGTTTACAGCCTAGAGAAGAAAGGCTTTGGCCCTGGTGTGGTGGCATAGGCCTGTAAATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTCGAGACAACCTGGGCAAT GT
L38517	137 G C ---	---	---	GGGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGACCTGAGCTGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGACTTGACTGGGCAACACAGCGTCCCCCAG CC[G/C]CGTCGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G ---	---	---	ACTTGAGAAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAAATACAGTAGTTCCTTTTGTATTTGTATATTT/GJCGCCTGA AGATCATCCCGCAAGCAGGCTGGAGGTGCCGTGGGCTGTGTTGCTGGGATTTAGTCTGTGCTGG GAG
L41268d	173 G A ---	---	---	CAAAGTTGCTCTCTGCCATGAGCACACAGTCAGGCCCTGAGGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGGTTGCCAGCTCCATGTACAGCAGCTGGAATCTGAAGCGTGAGTCTGCAT CTTAGGGCATCGCTCTCCTCACACCAAAATCTGAAC[G/A]TGCCCTCTCCCTTGCCTTACAAATGTCT AAGGT



U06641d	166 C T ---	---	CTCTCCTTTATTTACGATGGAGGGTTAAATGGAGGATCTCCTTTCTGTGACAAAACATCTTTC ACAACTTACCTTGTAAAGACAAATTTAAAAAGATCTTTTACAACTTACCTTGTAAAGACAAAT TATTTCCAGGCTATTTAATACGTAATTTAG[C]/JTGGAATTTATCTATGTCAATGATTTTTAAGCTA TGAAATACAAATGGGGGA
U09607	39 T C ---	---	GAGGCCTTATGAGGTCCTCTACTTCAGGAACACCCCAAT/CJGACATTCATTTGGGGGGCTCCCG TGGCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTTAAGGTTCAAGACAGATGGGCATATGTGCAG TGGGGCTCTCTGAGTCTGGCCCAAGAAAGCAAGGAACCAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82 T C ---	---	GAGCAGAAGGCAAGCGGCAAGATGAGTTTGGCGTTGTATTCAAAGGCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[C]/ACATCTGCCCGCCCTTCCAGCCCTTCCAGCCCCCTCTCTGTTCTTC ATTCATTCAACAAAATTTGGC
U10694	20 C G ---	---	GTGACATGAGGCCCATTTCTC/GCTCTGTGTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCATCTCTGGTTCCTTGTCTATTGGGTGATTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAAATGTTCTTTAATGGTCAGTTAATGAACCTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162 T C ---	---	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGCACAAGTTGTTTAAAC CTCTTTTTCAGAAAATTTCTCCATGGAGTAACAATATCTAGTTGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAAACAGCCAAAGAGAT[C]/JTTACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTACCTTCAGCA
U15555	187 T C ---	---	TTCTGTCCACTTTCACCTGGTTTAAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTTGGAGAAATTAATAAGCAATGCTGAACATCAGGAATTTGTAGATATCCGTACAGAGAGT TCCAGTAAAATTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[C]/JGGTCTCATAG CTCATATGCAGGATTCATCA
U17077	122 T C ---	---	TCCAATTTATGGTCCCCAAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAAACGGAAGATCCACT AAAACGTCCACGGGATTAACAGAACGTCCTTGCAGACTGAGCGATGACACCACAC[C]/JTTGTTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTTCTTTTCTGGGAAAACAACTGTCCTTGG AATTA
U18543	58 T C ---	---	GCACATGCAGAATAGACTCAGCCTATGTCTCTGATTCAGCTGGGTAGTTCTAGAACTTT[C]/JAGAAG CTCCATCTTTAATGTTTTATTGTTATGTCCTCCCTCCCGGCTTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGATTAGCAATTAGGCACCTCC AAGGCTTTAGTAGAGAGAGCC

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U25975b	164 C A ---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAAATTGCAAAAAGAC[C/A]AAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143 C G ---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAAC[C/G]AAGAGAAAAATTGCAAAAAGACAAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61 A G ---	---	CAGGGAGAGGTTATTACAAACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCA[A/G]TT TTGAGTGTACTGTGCCTGGTTGATTTTAAAGTAGTTCTCTATTTCTATCCCTTAAAGAAATTT GCATGAACCTAGGCTTCTGTAATCAATATCCCAACATTTCTGCAATGGCAGCATTCACCAACAAAA TOC
U28413	29 C T ---	---	ATTCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATTTTCTCATGTTTAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCTTGATJCC CAGATGTTGTGGCCTGGGAAAGCCCTCATTGCTACAGTACAAGTAAACAAAGTCGTTGTACCTCAGTT G
U30884c	89 A G ---	---	TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGACCTGCCGTATAATCTGTT CTTCTATTTCCACGTTAGCCA[A/G]TTGTTCTTGATGAATCTATATGATCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAAGT GCTGTCA
U30884a	34 A G ---	---	TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGC[A/G]GTGATGATTTTGGACCTGCCGTATAATCT GTTCTTCTATTTCCACGTTAGCCAATTTGTTCTTGATGAATCTATATGATCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAAGT GCTGTCA
U31216b	78 A G ---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCAATGAGACGGCTGCAACCAAAACA GCCGTCAATCA[A/G]CCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAGAGCCCTTTACAACGTAGAGGAGGAGGATGCCAGCCGATTGCGTTTAGCCCGCC TGTTAGCCCTTCCAT
U31216a	70 G A ---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCAATGAGACGGCTGCAACCAAAACA GCC[G/A]TCATCAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAGAGCCCTTTACAACGTAGAGGAGGAGGATGCCAGCCGATTGCGTTTAGCCCGCC TGTTAGCCCTTCCAT

U31416c	76	G A ---			AGTTGCCAGCTCCCATGTACACAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTGCTCTCTCTTGTCTTACAAATGTCTAGTCCCACTGCCTGCT GGAAAGAAACACACTCCTTGTCTTAGCCACAGTCTCCATTTCACCTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68	C T ---			AGTTGCCAGCTCCCATGTACACAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCTCAGCCACAAATCTGGTGCTCTCTCTTGTCTTACAAATGTCTAGTCCCACTGCCTGCTG GAAAGAAACACACTCCTTGTCTTAGCCACAGTCTCCATTTCACCTTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78	C T ---			ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCAACTCACATTGTTCTCTCC AGACCGCAGG[C/T]TCCCCAGCCTCAGTTGCTGGAGCTGTCACATGACTGCATCCTGCCTGCCAGG GCTGCAAGCAAGTCTTGTCTTATCTGGGGACGCTGCTCGAGAGAGCGCGAGAGCGCCGAGAAC ATGCCAGGTGTCC
U37690	54	A G ---			GACCACGCTGAAACCCACCCACCCGCTGTGCTGACCATGGGCCCTGAGCGTCTT[A/G]CCCCGAATTC ACGAGGCTGAGGCATCCGGAGCTGGCGTAATGCTGGCCGAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAGTCTTT
V00540	39	T C ---			TGAAACCGTTTCAACATGGAATGATCTGTATTGACTAA[T/C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCCTATAACCCAGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAGGCACACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106	A T ---			TCAAGAAGGTGACTGCCCTTGTATGATGGATGGGAAGATGAATGACTGTTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCCTGTGGTTTTAA[A/T]ATCCATAAGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCTAGAAATTTGGATTTCATCTCTGTTTTTCAITGCTCTCCTT GTAAACCTGAGATCATCAG
X52011b	148	C T ---			AGGAAGATCCCAACCGACCCCTTCTGGCCTAATCCTTTAGATTAGGTACATTACATTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAAGTTGCGAAATTTGCG AAATCTGTTGTGCA[C/T]GCTCAATGAAACGCCCTTTGGCTTTGGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118	A C ---			AGGAAGATCCCAACCGACCCCTTCTGGCCTAATCCTTTAGATTAGGTACATTACATTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAA[A/C]GTTGCGAAATTT GCGAAATCTGTTGTGACGCTCAATGAAACGCCCTTTGGGCTTTGGGCTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT

X54741	24 A G ---	---	CAGGCCACCTGCTCTCTCCACAG/GJTGACAGCTTCTGAGTACCCCTCTGTCCAGCCAGCTCT GGACAAATGGAACCTCCAGGGCTCCAGGACTGGGGCTTGCCAGGCTTGCAATAGCAAGGCCAG GGCACAGCTGGAGACGATCTTGCTGGCAGGGCTGGCTTGCTGCCAGCCCACTGCGGCCCTCTOC
X54869	99 A G ---	---	AAGCATTGCGTTACAGTGCATACATATTATTTCTTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATATGTTATTTGCTCT/GJATACAAAATCTAAATCAATATTGAAATAG GATGCACAAATTAATAAGTACAGACATCTAGCATTTGTGCGGCTCATTTGTCTCAACATGGTA
X66924	147 G A ---	---	GCCGTGCTGACACCTCCAGAACGAGGTGCTGGGCCCGTTCTGCTGGACCCCGGGAACCTCTC CTGCCGGAAGCCGAGCGGAGGATGGCCCAACTTCGCCCTGCCACTTGACTTCACCAATCCCT TCCTGGAGACTG/AJACCTGGTCTCAGGAGCGAAGGACTGTGAACCTTGCGCTGAAGAGCCAGA
X78932	62 T G ---	---	GAAATGTGAAGATGTGACAAAGCCTTTAAGGGTTGTACACTTGATTGTATATAAGATAAT/GJT CATACTGGAGAAACTCCAGAAAGTGTGACAAATGTGACAAACATTTAATTTCTCATACCTTA TTGCACAGGAAAGCAATTTATCTTGAGAAAAATGTATAAAGATGGAAAAGTCATTAATATCTGCT CATATCTTAACATCAGCGAGTT
X80026	25 T C ---	---	CTCAACCCATAACCTCAACCACATCT/CJTATCTCCACCCACATCCACACATCCACCTCCATCC CCAAACCATCTCATCCCAACTACAGCCCCAAACCCAGCCAGACTAATCCACAGCCATCCCCAA CTCATCTCATCCCAACTGCAGCCCCAAACCCAGGCCATCCCCAAACCCATCCCCAAAGCC AACTCAACACCATCC
X80197b	99 G C ---	---	ACCCAACTCAAGTCCAGGCCAGGCATCTTCTGCCCTGCCCTTGCTTGGCCCATCCAGTCCAGG CGCTGGAGCAAGTGTCTAGCTACTTCTCTG/CJACITTTGAAGACCCCTCCACTCTTGGCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X80197a	28 A G ---	---	ACCCAACTCAAGTCCAGGCCAGGC/GJCTTTCTGCTGCCCTGCCCTTGCTTGGCCATCCAGTCC AGGCGCTGGAGCAAGTGTCTAGCTACTTCTCTGCACTTTGAAGACCCCTCCACTCTGCGCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X85106	150 G A ---	---	GGCACCCAGAGTGACCAAGTCCAGGAGGGCGCGCCCTGCCGTGCTCGGTGTTCTTTT CAGCCCGGAGAGGTCTGACCTGGGGCTTCTCCAGCCTACTGGCCACGCTCCCGCCGCTCT CTTTTCTCCCAAGC/G/AJAAACCAATGGGCCCTTCACTCGCGTGGCGGCGGGGGCTT CTTTCAGAGC
X87160	128 T G ---	---	ACCACCAAGCATGGTCTAAGGACATGGATGGGTGCCCGCCAGACGTGTGCACAGGGACCCCTCTGCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCTT/GJGGG ATGCGCAGGAGGAGCCATCGGGTACTACGCAGCAACACTCACAACTGTCCAGGCTGAGATAAATCCC GGGA





1282	130	C T	---	---	GTGGATACCACTACAGTCTAATTTTCAGATGTTTTTCATTACCCCTAAAAGAAATCTTGTAACCAATTA GCAATTATTCCTCATCTGCCCTCACCCCGAGGCCCTACTCTTTATCGCTATAGATTTGGC[C/T]ACT TGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTTCTTTCACCTGAGAATA ATGTTTTCAAGGT
6810	68	C T	---	---	AGTATCACACATACCTTAATATATAGATATACACAATAATAAATCACTCCCTACCTTGAAAACTTT A[C/T]AGAAGCATTTTTAAATTTTACAACACAAGCTCAAACGACCTACAATAAGTCTAGTAGTCTG TTTACGTGCCAAGGGATAAGGCTGAACAATAAATTAAACCTTTAAATAATGCTATGAACAAGTACAA TTTTCTTTTGTAGTCTGCAGAGCAATGACCACCTAAGAAATATTTTTAAAGGC
6817	118	A C	---	---	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTGCTTTTGTATCCAGTTAAGACCA TCAGCATATACAACATCACTAACAATGTAAGTCTGAGGGTAAC[A/C]TGTGGATACCCCTG TGTGCTCTACTGGCCTCCAAAGGCATTGAGGGGATCATCAAGATGTTGGACACCTTGTGTTTCAATC TTGGTTCAGGTGCGGCCCTGTCAGATCGGCTTTTGGTTTGGTTGCTTAG
6819b	212	C	---	---	CCATTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAACACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTAGCAAA CAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
6819a	166	G T	---	---	CCATTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAACACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATTTTGTCTTAGC AAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
681xx	39	A G	---	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[A/G]TTACTATGGCACCATTTGGGACA CAGATTATATATGTCAGACACCAAGCAATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCATGGT TTAACAAGAAATGAACGCTAGG
6972b	149	G T	---	---	AGGATTCCTCTTTTCTTATGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTCTGGACTCTTTTGGTTGGTAAACTATTGATTATGC CACAATTCAGA[G/T]CCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCTCGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122	A G	---	---	AGGATTCCTCTTTTCTTATGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTCTGGACTCTTTTGGTTGGTAA[A/G]CTATTGATTA TTGCCACAATTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCTCGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

7598k	210 A C ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGCAG[A/C]
7598j	208 A T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGC[A/T]GA
7598i	192 G T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598h	144 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]ATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598g	142 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598f	120 A G ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATATTTCTTG[A/G]GGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598e	83 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTA[C/T]CAGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598d	77 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTA[C/T]GCTAACCGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTACAAAAGACACCCAAAGCCAA/GJAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAATATTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTACAAAAGACAC/GJCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAATATTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTJAJGJGATTTACAAAAGACACCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAATATTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAAATGAATGGGTGATGCTCTATCTTCTCAAGGTCCCAATAA/JTCTTGAGGTTCCCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAAATGAATGGGTGATGCTCTAJCJTCTCTCAAGGTCCCAATAA/CCTTGAGGTTCCCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTJAJTGAATGGGTGATGCTCTATCTTCTCAAGGTCCCAATAA/CCTTGAGGTTCCCT
8071	119 A G ---	---	AAATACAGAAATTTTATTAGAACTGTTTAAAGTAGAAAAACCCCTGTCAAGAAAGACCAGGTGG AAAATGGGTCCCAATAAATGGAATTTTAGGGCAACAAAAGTCTAAAGGCCJAJGJCAAAAAGAGA AATAGCACCACCTGTCAATTTGAACAAATGGCTAGTTACTTGCAATTTTGGCATTGTTAATCACTGAATC TGGGTTTCCCTCTGAATCCACACAGAGCATGCACACACATTTTATCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAACTGGGAAAATCCTGGATATTTGGCTTATCAGCTT TGACGCAAAATCCACTTTGCTGTAAJAJGJGTCATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGCATGCAAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTAATG
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAACTGGGAAAATCCTGGATATTTGGCTTATCAGCTT TGJAJGJGCAAAATCCACTTTGCTGTAAACGGTCATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGCATGCAAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTAATG
8498	84 C T ---	---	AGGGTTCAGGGTTTGGTTTAAATCAGGCTGCACACCTTTCAAAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAGJAJAATACCTTCAATTAATCGAAAAAGAAAAAATGCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTCTCTCTCAATACAGAACCCAGGAATGTAATTTTCTCAACTCAG

WI-18562	29	G A ---			CTAAGGAAAAATTTAATGATGGAATATC[G/A]JACAAATATTCACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTTGGGATAGAAATAGAATAATGTTTACAATGATTTCTTACATT TAGCATTAAATCAGAAACGA
WI-18618	51	A C ---			ATAGCAGACTTTTAAATCAATGCCAGAGACAAAAGTGAGGCCGAGCTAAGAAC[A/C]JGCTCAGCTTCG TTACAATGAAGAAATGGTTTCTTTCGATGCAAAAGTATAATTGTAAACACACAGTGCTCGCACAGTTC AC
WI-18683	22	C T ---			TAAGCTGTTTCAGGACTGGACTC[G/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCTCCAAAGCCTGCCTGCAGT
WI-18520	75	G A ---			GACTTTGGTGATTTAATTGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]JCCGGAGTGGTAAATAGTACCTACTGCGCAACAAACACGGGCATCCACTCTGTCTTCAA TGCCTCTCCGTGAGAC
WI-18563	94	A G ---			AAATAAGTTTTTATGGCACACAGCCCAAGCCCACTGGGATGACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	T A ---			GTCTATTCAATTTAGTAGACCCATTTCATTCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC TT[A]GTGCCATAATTTAATCATAGTCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94	G A ---			AACCTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAAG TGGTAACAGGTACATAGGTAACCAA[G/A]TATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71	T C ---			AACCTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAAG TGGT[C/A]ACAGGTACATAGGTAACCAAAGTATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96	A G ---			AACCTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAAG TGGTAACAGGTACATAGGTAACCAAAGT[A/G]TATAGCTTATTGGTGAATCTTCATCCT
WI-18619	44	G A ---			TTTATTACAATATTAGGTGGCACATAACTAACAGCTTCTG[A/G]ACAGGAGGTAACATTCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAACTCGAAATA
WI-18715	76	G A ---			TTATTCACAAAAAGTGATATTGCAGAGGTCTGGGGCTGTACATGGGCAGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGGAAGGTTATTTTAAATAAAAAAATAA TGGAGCTACAACACCCCC
WI-18535	107	G A ---			GTAATAAAGTTTTATTGGCACGCCACGCTCGTTTCATTTCATATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTAAAGCAGTGGTCCCAAC CTTCTGTGTOOCCGIG
D17525	107	C T ---			AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTTACTAGTTTCTGGCAGGTGAC TTTATCTCTCTTCGAACTTCAGTTTCTTCATAAGATGGAAG[C/T]GCTATACCTACCTACCTCGTAAAA GTCTGATGAGGAAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGCATAGCATACTGTTT TCAATAAATGCACCTTAGCAGAGGTGATGTGTCTACCGCAGACGAAG

DWU-133c	313	A G	---			TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACITTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGAAATATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGITTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C	---			TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACITTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGAAATATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGITTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T	---			TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACITTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGAAATATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAAC[C/T ITCCAATTCAGTAAATGGTATCACTCGITTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T	---			ATGAGATCCTTTAAATCCTTCCATGAAACGTTTTGTGGTGGCACCCTCCTACGTCACAAACATGAAGTG TGTTTCTTTCAGTGCACTGGGAAGATTTCTAC[C/T]GACCAACAGTTCTTCAGCTTCCATTTGCGC CCTCATTTATCCCTCAACCCCGCCACAGGTTTATACAGCTCAGCTTTTGTCTTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAAGGATTCATGTGGAATATAAAGAT
DWU-387	169	G T	---			GTGTATAAATGCAACTGTTGATTTCCTCAACATGGCTCACAATTTCTATCCCAATCTTTTCTGAA GATGAAGAGTTTAGTTTTAAACTGCACTGCCAACAAAGTTCACITTCATATATAAAGCATTATTTTAA CTCTTTGAGGTGAATATAATTTATATTACAATG[G/T]AAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTCACCAAGTATCAAGTAATAACACAAATGAAGTGTCAATTATTCAA
DWU-447b	172	--	---			ATTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAAGTGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAAATTAATTAGTTTATTAGAGCACAAAGCTTAGCTAATCAA CCATTATTTTCAITTTGTTTGTCTAAGAGGATTGANAATCAGTTTAGITTTAATGTCTTTCTGTAG GCCTTTCTTCTTACAATGAAGAGATGATTCITCTAGTTTATGGTTA
DWU-447	85	A G	---			ATTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAAGTGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAA[G]ATCACTGTAAATTAATTAGTTTATTAGAGCACAAAGCTTAGCTAAT CAACCAATATTTTCAITTTGTTTGTCTAAGAGGATTGANAATCAGTTTAGITTTAATGTCTTTCTG TTAGGCCCTTCTTCTTACAATGAAGAGATGATTCITCTAGTTTATGGTTA
DWU-476	63	C G	---			GTAATAATTCAGTTTTTTCCAGTTCCTCTTTTGTGCTGCTTCTCAATTAGCGTTTAAAGTGAG[C/G]AT AAATCAACTGTCCATCAGGTGAGTGTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTTT

DWU-505	67	A T	---	---	TCATACTAGGCGAGTATCTCTCTAGCTAGTGGCCCATACAGAAAAATTTCTATCACCATACAAAAATTA[ A/T]TGCAGATATTTATGTTTTAAAGCACAGGTGTACCGAAAACTGTGAAAAGTCTGAATTTATGGGTT CTATGCATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACITTTGACTTTGAGCTTTAAACTTTTAA
DWU-512	131	A G	---	---	AAAATCCAGGCATTTTCAATCTGTTTTTCATGATTTATAGAGGGTTTACAAAAAGTGCCACTTATTAA AGAGCTTCCACAGTGAAGATGGAGAGGTGAACCTTGCTTTGAAATATTCAGATGTGTTTGGTC[A/G] TGCGTATGGCAGTGAGCAGGTATGTTTGTCTTTTGTCTTGCACTGAAAAATTAATTTGCTATCAAGAGC AAACTATGAACGGTTTTTTATCAAGATGTCCTCAGAGTGAAGATGCCGAG
DWU-525	97	A C	---	---	AACTGCATATAGATAATTATCCAGGATGTGTGGCTCATCTTTTCAGCTTGTCTTCTACTGTTTGTGA ATATACAGTTTTTGTAAACATATGATTGA/CJAAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAATAACATATCTTGTCTTTCACAAATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAATCTAGTCTCTGATTTGG
DWU-59	94	C T	---	---	CATTTCTTTGTAAAGGTAATGGACTCACAAAGGGGAAGAAACATGCTGAGAATGGAAGTCTACCCGG CCCTTTCTTTGTGAACGTACATTTGGC[C/T]GAGCCGTTTTCAGTCCAGGTGGCAGACTCGTTTTTG GTAGTTTGTTTAACTCCAAGGTGTTTTACTTCTGATAGCCGGTGATTTTCCCTCCTAGCAGACATG CCACACCCGGTAAGAGCTCTGAGTCTAGTGTTAAGC
EST11	68	C	---	---	CTTGATCATGGGTGGAATTTTGTGTAICTGGGCTTCATGGGATGCATAAAAAATTTTCCAGTTGGTAAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63	C T	---	---	CACACTGGCATCTAGGCCTTCGCCTGCAATTCAGAAAGGAGAGCCAGGTCCCCCTCCTGGAGAA[C/T]G CTGCGTTCCCGCAGCCCCACACCGGCTTTGCACACAGGCTGTTGAGGCGAGGTTGGTAAAGACGT AGCTGTAGACCCAAAGCAACCAAGCCCTGGGACCCCTGCGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGGTCACTCCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40	A G	---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[A/G]GAATGAAAGTGCAACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97	T A	---	---	TTCCAATGTAAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTAATCTTTTCATAA[T/A]CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27	T C	---	---	TTCCAATGTAAAGAGTCAAGTACCAAGTT[C/J]AAACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTAATCTTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72	C T	---	---	TGTAAGGTGACTTCTATAAGCTTCCCTAAAGTGTCAAACTTTTCATTTACTGAGATTATTTTCAGGCCAAT GTGTC/T]TGTGGGCTGAGATTGATTATCAGCTGGGTAAGTTAACCTGTCTCTGTTTCA

WI-18063	105	G A	---			AGGCTTTAAACTGATAACAATTGCCTTTAATCACAATACAAAACCTGCACTTTCATTCCTTCCTTC CCATGTTTCTGATTTGATGTAACTTAAATTTGTG[A]TCCCTTTAACAAATATACTGAGCTGCA AGTTGAAGATCAGAGAGGTTATGGTTGGTAGCTGAAGCTCAGATTCAGATTCAAACCTGGTCCAGTGTG TTGTTTTTTCAGCATCAG[A]TGTCCACTAGCCAAAGTTGATCTCTGCAGTATCTACATGTGGT CCAAAGCTCACTCAGTATTTAATCACTGCTAATTCATCCTTTTGTAAATTCATCAGACACTGTGGT TTTCATCTCTAGAAGTTTGAATTCAGGCTTTTATACCTTCCATATCTCAACTTGTTAAGC GCAATCTGTAAACAGTTTGGTAGTGTATTACAGAGGAT[C]TTGTAAATGGATTGGAGTACTTAC CACTATTTCTGCTCTGAAATAGTTCACTAACCAAACTACTGACAACAGTTTAAATTTGGTTCTT TTCAAGATAAATTACAATTGAAGGGGACCAATAATTCACCTTTTAAATCGAAAATAATCTATATAC[ T/G]CCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAGAGGAAAA GCATAGGGTTGAGGGGTGTACAAGAGGAGAACCAAGATTCAAGTCCATGCCCTGGAGGTAGTCTGGGG GT[C]CGGCGGGATGGACACACAGACAGACACATAGATCTGGCATCTGATAGCAGGGCATAACAG TCAATCTGAAAACCTTGCCTGAAGCCAGCATGGGGT[G]TGGGGAGGTGATTATGGCTGGGGAAGATG GGCACTCACCCGACAGCAGCATCTAGCACCAACAGTACAGGGGACGTTGAGGTGGCAGAGGGCTTT ACAGATGTCAGTTGTTGAATTGGCCCATTAAGTATGGGGCTTTCTTGTAAAAGTCATCCAAA AGGCTTGGCAAGAGTTTGTATACACGGAGGACAGAGAACATGA[G]A]CTGGGGAGTAGGCTCT GACAGAAGGTGGGCTGTC
WI-18078	86	A T	---			GATTTGAAGGGATTGCTTTATTAACTG[A]TGAAAAGCGTGATAGAGGAACTGTTTAAGATAAACAA CTTATAAATACCTCCCAATTTGTAGAAGTGAAAGATTG
WI-18091	90	T C	---			TAGGAGGGAAAAGAGGTTGGGCTGCCCTGAGGCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAAGC TTCTTACTTCCCCCATAGAT[C]TCTGACAATGTGCTGCAGAAAGCCTCCAACTGGAAC
WI-18119	38	T C	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCCAAAATTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18142	66	T G	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCCAAAATTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18178	68	T C	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCCAAAATTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18244	35	G T	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCCAAAATTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18245	115	G A	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCCAAAATTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18261	26	G A	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCCAAAATTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18268	88	C T	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCCAAAATTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299f	107	C A	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCCAAAATTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299e	101	A G	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCCAAAATTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299d	77	G A	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCCAAAATTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299c	67	T G	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCCAAAATTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG

WI-18299b	52	G A	---			TCACAAAGTCATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACTTG[G/A]TTTGCCAAATTTT TTATCTATTTGGGCTGAGAAATCCACAATTTGAAGAATCTTTGCCAATATTGACATATTCTG CAG
WI-18299a	48	C T	---			TCACAAAGTCATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAA[C/I]TTGGTTGCCAAATTTT TTATCTATTTGGGCTGAGAAATCCACAATTTGAAGAATCTTTGCCAATATTGACATATTCTG CAG
WI-18307	76	G A	---			TCAACTTGTACCAAGTTTAGCAGCAAGAGGATACITTCCTTAGAGACTTTCAGTGGACTTAAACTCAG TTTCCGCTG[G/A]TGCTATGTAAAGCATCCAGATGGTTTATTGTACTCTGCAATCTGCTTGGTCAC
WI-18324	72	C T	---			TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAAACTCCGGGGTGGGTACTGATT TATC[C/I]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48	T C	---			ATGAAAGTCACCTTCAATCATAAGGGTCAAGAGAAAGAAATGTTTTAGAT[C/I]TAATCTATGAAAA GGTGTATCTGCTGCAATTTAAGAAACAACACAAAGTCA
WI-18395	77	G C	---			TCITGACATGATCTGTGAAATAACGTGATTGTGGTTGAAATTCCTGGAAAAATTTGAAGATAAATG ATTATTCAAG[G/C]JTGTCATTGGTTTATACATATCTCCTCTCTTAAATGCAAAAGCTATG
WI-18398	62	G T	---			TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAACAACACTCAAGGGTT[G/T] GATAACATTGCCAGTATAACCATATTCAAACAAGCAGCAGAAATTTGGAGGATAATTTGTT
						CTCGTTGGTATTCTCTCATCC[C/I]TTCCCTTTTCGCTCTTTCTAAATTAAGAAAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACATTTAACTTATCAACTTGTACAAAGTC AATGAAAA
WI-18396	21	C A	---			AAGATGGGAAAGAGGAAATC[C/I]TTTTTCTTACTAGAGATTTTTCCTTTTAACTCTTTTCAAAAT TCAAGGATCATCAAGGAGCAGGTGCAGAAAGCTCTGGGCCAGAGGCCCCCAAGTGCTA
WI-18409a	20	C A	---			AAAAAGGAAAAAGAAAGGATGGAGTAAGAGAGAGAGACAGAGAGGAAACAAAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAAAGGAAACACAAAGAGAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18442	62	C T	---			TTGATGTTAATACTGTCAATCTGGGATCGGCTAAAAATG/AJAAAGCATAGTTATTATTAGCTTTGG TATATCTCGACAGATTAAACAAGTAAGACATATATCAACCTCATATTTTCCAACCA
WI-18452	38	G A	---			ATATAAGCTGGAGACTGTGGAGGTGAGAGGAGTGGGACTAGCTGTTGAAAGAGAGAATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAACA[C/I]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
WI-18489	102	A C	---			CTGGTGGGAGGAAACAAATTTGGGTATATTATACAAATGGAAAAACTCTTCAGAAATAAGAAAGGAA CAAACTGAAATCACACAACATGGACAAATCTCAAATCATATGCTGATGGAAAGAAACCATTCA TAAGAATACACAGTACAT
EST5b	93	A	---			---



EST5	93 A ---			CTGGTGGGAGGAAACAAATTTGGGTATATTATCAATGGAAACTCTTCAGAAATAAGAAGGAA CAAACTGATGATCACACAACATGGACAAATCTCAAATCATTTATGCTGATGGAAAGAAACCATTC TAAGAATACACAGTACAT
EST6	48 C ---			TTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAAAGCTTTCTTCCTTTTGCACAAAGACAAAGCAAGCAACATTTTGCATTAGACAGAT
EST8	158 A ---			GGACAGGACCTCTATTCCCGCTGTGCAGCAGCGGCTGATGGACTGAGGCCCCAGGGATACTGGGOC CTCTCTCAGGGCGCTCCAGGAACCCAGAGCTGTCTCTGTTTGGTTTCCCTAGAGCTGTGGGCCA GATAGCTGTCTGAGTTGCAAGCAGCATGGAGATTGGACACTGTGTCTTTTGGTGGGT
WI- 18740c	104 G T ---			TCCTCATTGTGGGGATGATGAGAAGAAATGATTTGGGAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCAITTACCATCATGTATCCAGTAGTG[G/T]ATAATTCATTTTATGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C G ---			TCCTCATTGTGGGGATGATGAGAAGAAATGATTTGGGAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCAITTACCATCATGTATC[G/G]AGTAGTGGATAATTCATTTTATGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 C T ---			CCAAAGTCTCTGTCGCTCAATAAGAAAGTTTGGGATGGGAGAGAATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCCTTCAATTTACAGAGGTAGCACA[G/T]GATTCCAAACAAACCCCTTCCCC TTTTTAAATGATTTCTGTTCTAATGCCATAGATCAAGGCCCTCAGAAACCATTTGTGTCTCTCTT TGAAGCAATGACAAGCACTTTACTTTACGGTGGTTTTGTTTTCTTAT
WI-18746	114 G A ---			GCCAGCAGCTGAAGTCTCTTTCTCTCTCGGCTGGAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGATCTTGACCGTTTTTATATTACTTTTGTAAATATCTT[G/A]TCCACATTCCTACTTCAGCT TTGGATGTGGTTACCG
WI-19112j	212 G A ---			CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGGTTACGGCCCGGGGGAATATGCCAAGG GACCCCTTAATGGAAACACAGATCAGTAGTGTCTATCTCATGACAACCCACAAAGAAACCGACACAA TCTTTTGCAGATTTCTTCTAGTGGCTTAGAAACATGGCTTTAAGAAACACGGTGATATCTTTGAG GGTGACAAGGC[G/A]TCTCTTCAACAGTCCATACCACTGCTTTGCTCTAG
WI-19092	232 A C ---			TGGTGGCTGGCTAGTGTCTACAGAACATAATTTGCCTCTATAGAAGCTATTCTTAGATCATGT CTCAATGGAACACTCTCTTCTTAGCCTTACTTGAATCTTGCCCTATAATAAGTAGAGCAACACAC ATTGAAGCTTCTGATCAAGGCTCTGAAATTTTCATCTTGAATGTCCTTTGATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTTC[A/C]ATGATTAGCCGTGTAAC
WI-19057i	175 G A ---			CCCATTTATTAGGCCAGTGTCTCAAGAGTAGAGGAGCGTCTACTGGTCTTTCAACTCCTTCA GTCTCTGACGGCGGACTTACCCTGACAGCGGAAGTGTATGTACGTCAGGCAACCGCAGCCACTG TCTTCATGCAGGAACCAAGTGCCAGATCCCAAGCTC[G/A]TCTCTTCACTTGGTTTGGCCACA

WI-20103	168	C T	---			TGGGACTTCCAACTCAGAGGATGTGGGAATCCCAGCTCAAATGATACAGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGAAGCTGGGTCTCCCA[C/T]TTCATCTGCTCAAAGCTTCTTGAAGGAGC TGGTTGACTTCAACTTGGTAGAGCTAGCTCATCTTTTTCAGTCAACTGGGA
WI-20441	111	G A	---			GCCTTACCCATTTTGCACATATACATATGCACCCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAAATCTTGTAGGACAAGAAATGGA[G/A]TTGAATAAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCGTTTTTCTACTACATCAGAGGCCAAATAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116	A G	---			TGGTTACAAAACCTAAGCCCATATACAAAATAGGAACACATTTAGATGCCTCTTTTGAAGAAGCGT TTTAGTCTTTTAAACTGAGTTTAAAAAAAATAACAATGCAATTTT[A/G]ACACTGTTTTTGA ACTTAAAGTCAGCAATA
WI-20613c	165	A G	---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATGGCATGGGAGGAGGCGAGTTAGAAAAACATCTAAAC AGTCTCTTAGAAGGCCAATAATAAAGTTGGAA[A/G]AAGGGAGTTTCCACGCGCAGGTGGTGAGC TGC
WI-20613b	156	A C	---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATGGCATGGGAGGAGGCGAGTTAGAAAAACATCTAAAC AGTCTCTTAGAAGGCCAATAATAAAGTTGGAA[A/G]AAGGGAGTTTCCACGCGCAGGTGGTGAGC TGC
WI-19984	47	A G	---			CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAAAT[A/G]TATAACATTAGAAAA GCAAAATCTTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAATGAAGGCAGTTTCCAAATCTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	T C	---			GCCAGTTGGAATATGGCTATACGAACCAAGAGTGATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTTCTTGGAACTCTGCACCGACTGTCCATGCTCTGTGGGACTTACACATTCAAGTTTGACAG[ T/C]TGAAAAACCAACTGGAGCTGCTTTTCCAAGAATGTTCTGTGCTTCAATAGGAATCCATG TTATTCTTTCTTGCTTAAGCTCTTATATCTTTCAAAATGACCTAAGCTGA
WI-18846a	49	G A	---			GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCCT[G/A]AAGCTGGGAGCGT GGGCTCAGCAGGCTGTACCTCCATCCCGTAAGACCTCCTTCCCTTCTCAGCAGGCCCAACATG GCCAGACTCCTT
WI-18959	123	G A	---			AGCAGTGGCCTTATGTCATCCCAACACCGCTCTTGACCAGGCTGCCCTCCCTTGTGGCAGCAACGGC ACAGCTAATTCTACTACAGTGTCTTTAAGTGAAAATGGTCGAGAAAGAGGCACC[G/A]GGAAGCCG TCCTGGCCTGGCAGTCCGTGGGACGGGATGGTCTGCTGCTGTTGAGATTCTCAAGGAGCGAGCAT GTCGTGGACACACACAGACTATTTTATAGATTTTCTTTGCCCTTTGCAACC

WI-20146	31 T C ---			---	TGAGTCTTCTGTAATTCATTGAGCAGTTAGCT/C/CJCAATTTGAGATAAAGTCAAAATGCCAAACACTAG CTCTGTATTAAATCCCCATCACTACTGGTAAAGCCTCAATTTGAATGTGTAATTCATACAGGC
WI-18922	74 G A ---			---	TAGGAATTGGTTTACGCCCTGAGGCAATTAGACACTTTTGAAGATGGCATAACCTGTCTCACCTGGAC TTAAGC/GA/JTCTGGCTCTAAATTCACAGTGCCTTTTCTCCTCACTGTATCCAGGTTCCCTCCACAGAG GAGCCACCAGTTCTC
WI-18763b	53 A G ---			---	TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTA/G/JTATTAGAATG TACCATAATTTTGTAAATTTATGTTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTTTTTGCCAA
WI-18763a	38 A G ---			---	TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGA/J/GJTGACGATGATGTAATATTAGAATG TACCATAATTTTGTAAATTTATGTTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTTTTTGCCAA
WI-18771b	75 G A ---			---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGTGCCTAG/J/GJAGATGTT AACAGAA/G/A/AAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGTGCCTAG/J/GJAGATGTT GGGAACAGAGAAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G ---			---	GGGAAAAATTTGAGACGGAATACCAATCTAGGATTTTGGTCTTGGTGTGTAATGAAATCTGAG GCC/T/CJTGATTTAAATCTTTCATTGTATTGTGATTTCCCTTTAGGTATATTGCGCTAAGTGAAACTT GTCA
WI-18820	70 T C ---			---	ACAAAGTCTGTAGCCOCTCACCTTTCTGTTTTCACITTTGCCAATGTA/C/JATCGGGTTGGTTT TCTTGATATTATTAACGGTTGTGGTTTCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18742b	51 C T ---			---	GTGTGTCCAAAAATGGGTCTGCTCCTGCTACCTTGACCGCTTCCCTTTCTCTGCTTCTCTCCTCATCA TCATTTCCCAACAACATCCTCTGCCA/C/JACACAACAACAAACGTAAGTTTCATTTGGGCAAAAATTGA GC
WI-18882	94 C T ---			---	TATAAGCCGAGTCACCAGGAGGCTGTCTGGCCACAGACAGAGGGGCTGCCTGTGGAGCCTGCCACC GGCCCCGGCAGTGCAGTCAGCGGGAGGAGGCTGCCGTTCTGCCAGTTCTCCTCACTGGGGGACCC AGCAAGGCCCTTCTCACTGGGTGGTCAAAG/G/JTAGTCACCTTGGCCTGGTGCATCCACAGAGGA TGTTGTTCAAACAGAAATCTTTTAAACGACTGACCTTCTTTAAAAACAGA
WI-19970b	167 G A ---			---	TATAAGCCGAGTCACCAGGAGGCTGTCTGGCCACAGACAGAGGGGCTGCCTGTGGAGCCTGCCACC GGCCCCGGCAGTGCAGTCAGCGGGAGGAGGCTGCCGTTCTGCCAGTTCTCCTCACTGGGGG ACCAGCAAGGCCCTTCTCACTGGGTGGTCAAAGGTAGTCACCTTGGCCTGGTGCATCCACAGAGGAT GTTGTTCAAACCCAGAAATCTTTTAAACGACTGACCTTCTTTAAAAACAGA
WI-19970a	126 T C ---			---	

WI-19067d	202 T G ---				TATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGAGCCTCCCTGGCTGTGC ACATTCCTCTCTGCTCCCGAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCTGGAGATGTTGTAGGGGTTATTTTTTTAATAGTGTTCATAAAGAA[7] GJACATAGTATCTCTCTCAAGACGTGGGGGAAATTATCTCATATC
WI-19067c	153 G C ---				TATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGAGCCTCCCTGGCTGTGC ACATTCCTCTCTGCTCCCGAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCTG/CJAGAAATGTTGTAGGGGTTATTTTTTTAATAGTGTTCATAAAGAA ATACATAGTATCTCTCTCAAGACGTGGGGGAAATTATCTCATATC
WI-19067b	151 T C ---				TATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGAGCCTCCCTGGCTGTGC ACATTCCTCTCTGCTCCCGAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCTG/CJGGAGAAATGTTGTAGGGGTTATTTTTTTAATAGTGTTCATAAAGAA ATACATAGTATCTCTCTCAAGACGTGGGGGAAATTATCTCATATC
WI-19067a	57 C G ---				TATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGAGCCTCCJGJCTGGCTG TGACATTCCTCTCTGCTCCCGAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTT CTCTGGGCTCTAGGCTCTGGAGATGTTGTAGGGGTTATTTTTTTAATAGTGTTCATAAAGAA ATACATAGTATCTCTCTCAAGACGTGGGGGAAATTATCTCATATC
WI-19106	247 T C ---				TTAATCCAGCCCTACCTTGTAGTATTTAGGAGACAGTCTCAAGCACTAAAAGTGGCTAATTC AATTTATGGGTATAGTGCCAAATAGCACATCTCCACGTTAAAGACAGTGGATCATGAAAAGT GCTGTTTGTCTTTGAGAAAGAAATAATTGTTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGGCCATAGCCTATAATTGGTTAGAACCTCCTATTTTAA[7]CTGG
WI-18944	147 A G ---				CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAAAGTTATTATGAGCTGAAACAAA AATGCCAGAAAGGATAATATTGATTCCTCACATCTTTAACTTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAACJAGJTGTTTAAATTTACAAATATAAGTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTTCAATTTCTTTCTTAAATAATTTAAGTTT
WI-18952	232 G A ---				CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGATGTTTCATAATACATAAA GTTCTGTAAATTACAACTAAATATTATGCCCTCTTCTCACAGTCAAAAGAACTGGGTGGTTGGT TTTTGTTGCTTTTTAGATTTATTGTCCCATGTGGGATGAGTTTTTAAATGCCACAAGACATAATTA AAATAATAAACTTTGGGAAAGGTGA[GA]ACAGTAGCCCCATCACAT
WI-18932d	177 C T ---				CACACCTCATGTAGCCTCACGAACTGGAATAAGCCTTCGAAAAAGAAATTGCTTTGAAGCTTGTA TCTGATATCAGCACTGGATTGAGAACTGTTGCTGATTTGACCTTGTATTCAAGTTAACTGTTCCC CTTGGTATTGTTTAAATACCTGTACATATCTTTGAGTTCA[CT]TTTAGTACGTTGGCTGGTCA CTTCGTGGCTGAGGTAAGAACGTGTTGTGGAAGACAAAGTCTGCGCTTG

WI-19042	193 A C ---				TTTGTGAGTTGGCTCTCGCAATGCCATCAGTAGCATCTCAGTGGTGTGAAGTTGGAGATAGATG GATAAGGGAAATAGGCCACAGAGGTGAACCTTTGTGCTTCAAGGACATTTGGTGAAGTCCCAACAG ACACAAATTTACTGCGACAGAACTTCAAGCATTTGTAATTTATGTAATAACTCTAACCA/A/CJGGCTG TGTTAGATTGATTAACTATCTCTTGGACTTCTGAAGAGACCACTCAAT
WI-18984	208 A C ---				ATTGGCCCTGTACAGTTTGCTATTATAAATTCATTAACACACTACAGGTGTTGAATGGTTAAAA TGAGGCCCTCCAGTTCAATTTTCTGAGTGTGCAGACAGCTATTTCCGACGTATTAAAT GTAACCTATTATGAATCAGAACGAGTAGACAGATGTTGGTGAATACAAATATTGTGATGCATT TATCTT/A/CTATAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGAAT
WI-18851	90 T A ---				GCTTCAATTGGCGATTGATTGAGTGGCCACAATGTAAACAGGGTGGTAGTTGTACTCATTTTGAAT ATACCTTTTCCCTTATTGTATTCT/A/GTAAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---				TCAACTGCAGTTGCTTCCCTCCCTATAGGGCTGGAATCTGTAGGAGCCCTCTCTCGGAGGCC ACAGAGGGT/CJGGGGGTAGCCATTGTGCAGTCATGCCCCGGGGAAACTTGGCAACCTTCGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---				TCAACTGCAGTTGCTTCCCTCCCTATAGGGCTGGAATCTGTAGGAGCCCTCTCTCGGAGGCC A/C/TJAGAGCTGGGGTAGCCATTGTGCAGTCATGCCCCGGGGAAACTTGGCAACCTTCGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---				ACTCCTCTGCTGCTGCCAT/CJ/ACTGTCTCTTTGAACACAGGAAAGTCACAGATTTAAAGAGAA GCAAAATTAACATCCTGAATCGGGAACAAGGTTTATCTAATAAAGTGTCTCTTCCATCACGTTG CTACCTTACCCACACTTCCCTCTGATTTCGTGAGGACGTGGCATCTACTTACGTACGTGGCATAAC ACATCGTGTAGGCCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---				TGGAAATTCCTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG/CJTTAGGGAAACATTCATCCTTGAGTCAAAAAATCTCAATTCCTCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---				CACGGTTCTCTGCATCGTTACAGAGCGCCTTCTGGTCTAGCCAGCCCTGTATGCCGCGCAATA TCCCCAAAGCTTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCATTTTCTGGAGGGGTC CCCTCCCTTTACGAACAC/A/GJAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---				CACGGTTCTCTGCATCGTTACAGAGCGCCTTCTGGTCTAGCCAGC/A/CCTGTATGACCGCGCAA ATATCCCCAAAGCTTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCATTTTCTGGAGAGGG GTCCCCCTCCCTTACGAACACAAAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19054	66 T C ---				TTGAGGAGGTGGGGTGAACCTGCTCTTGGCAGGATTTGTACACTGCATTGCTGGGCTGTGTTCTT/ CJGGGCTCTTCTGGACCTTGACCCGTGGATACAGGCCATGTGCCATGTGTTGGGTCTGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---	---	AGGCTGTGGCTTATGTCAACCAACAGAGGGTCTCTGAGAAGTCTGGCTGCCGTGGGATGCCCCCTGCC CCCTCCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGGAAGCAG/GJTGCTTGTGGCCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCCCTCTGTGGCCACCAGGCACCTACGGCTTCCTCTCC AGATGTGCTTTGGCTGAGCACAGACAGTCAGCATGGAATGCTCTTGCCCA
WI-19016b	184 C A ---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTTAATATGACATGGTAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGACTGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTTGGGGCTGGATAGTCTCTGTGTGGGGGTTTGTCTTGTCACCTGTAG
WI-19016a	161 C T ---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTTAATATGACATGGTAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGAG/C/JTGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTTGGGGCTGGATAGTCTCTGTGTGGGGGTTTGTCTTGTCACCTGTAG
WI-20096	21 T C ---	---	GGTTTGGGGCATTTATTCT/JCJGATAGAGACTGGCACAAAGCTTTGGGCTAAGGACACCCCGCCCC ACCCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGGTAACTCCAAGCCATG AGTAAAGATTAAAGCAGTTACTTTTGAACAAAGGAAGTGCAATAAGCAACTCAGTGTGCCCC CTTAGGGTGGGAGCTCTCC/CJ/CTACCACTCCCAAGGCATCAITTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAAT/JATAAGGTAACTCCAAGC CATGATATAAGATTAAAGCAGTTACTTTTGAACAAAGGAAGTGGCATAGCAACTCAGTGTGT GCCCCTTAGGGTGGGAGCTCTCCCCCTACCCTCCCAAGGCATCAITTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	TCCTCCAGCTCTGTATCCTTGTCTTGAGGGTCTGTGTACGGCCCTCCAGGCATGGTTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAAGCCAGCTCTCTAGAGGCTCCA/G/JTCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATTTTGTAGCGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCTCCCAATGTCTCCCGGGGG
WI-20860	224 G A ---	---	CTCTCCCTAAGGAGCCTTGGCCTTGACGCCCATTCAGCAGGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCTCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTTATCCTGCTCTCCT CCCCAGTGTGTACACTTGGGCAAGCAGAGTGTGGGAGACCCAGCCTTGAGAGCTCTTGTAGACC GGAAGGAAGGGCGGTCA/TT/GA/EGGTGATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	GACGTGGACAAAGGAGGTTTAAATGAATCTTTGTTTGT/JCJCATGTTCAAAAAAAGAGATTAAAT ATTTTGTGACTGCATCTGTAATGAAGACACTCAAAAGCCATGTTTCCAACTTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTTCGGGCATTGCTGCAATATCTCGGCCCTCAAGTGGGAGGCCACGTG GGAACAAGGCCCTCAGAAACAAGGACATGCAGCCTCCCTGAGCCAGTCTCT

WI-19766b	93 A G ---	---	TGGCCTCAATGACTGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGG AGATGAACCATAGGAGCCAAAGTC/GJGACAAACAGAGAAGGCACACCAAGCCTGAAACCCCTC CGGACACAGCAGAGTACCAGCTGAGGGATGTCCCTGGAGGTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTCACTCTCTCTACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---	---	TGGCCTCAATGACTGTACATTGGAGAAGCT/GA/JGACAGCATCCTTTCTGTGGTGGCAGGGC AGGAGATGAACCATAGGAGCCAAAGTCAGACAAAGAGAAGGCACACCAAGCCTGAAACCCCTC CGGACACAGCAGAGTACCAGCTGAGGGATGTCCCTGGAGGTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTCACTCTCTCTACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---	---	CTTCTCTGTTGGCTTGCATTTGCGGATTGGAAAAACCACTTGAAGAAGGGACTTTCTCTGCAA AACCTTAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGACTGA/C/GJAAAGC TTAGAAAGGAAGTGAATTCCTTTGAATATGATTTAGGGCGGGCGTGGTGGGCTCAGGCCT TATTAATCCAGGACGTTGGGAGGGCCCAACGCGGGTGGGATCACTGA
WI-20512c	59 T G ---	---	CTTCTCTGTTGGCTTGCATTTGCGGATTGGAAAAACCACTTGGAGAAGGGACTT/GJTCCTG CAAAACCTTAAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGC TTAGAAAGGAAGTGAATTCCTTTGAATATGATTTAGGGCGGGCGTGGTGGGCTCAGGCCT TATTAATCCAGGACGTTGGGAGGGCCCAACGCGGGTGGGATCACTGA
WI-19599	230 C G ---	---	GGCTTAAATCCCTCTGTTGGGACTGGTCTCCAGTTACAGCAAGGATCGCACCCCTTTCC ATAACCCCTTCTACATTGGAAGAGCACACCTTGATACAGAATGGTCCGTGAAGTCTTTTAAACG GACAAAGGTAATCACAGCTACAAACGTCATGTTGGCTCACACGTAACCAACACACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGGCA/C/GJTTCCAGAGTAACACTGCTA
WI-20679	82 T C ---	---	TGTTTGAAATAAAAAATTCATGGTCTTAATTGAAGTGTATGTTACTTTCTTTAGAATATCCTTTT TTCATTAAATAAT/TJCTAAACCACTCTATGTGTTCAACCTCTGTTTAAACATAAGATATGGGT TTTTGGAAGGCCACAAAGTCACAGCTCCATGAAGTGGCGAATTGGTCTTGTTTGGAAAGCTCTC CAGGGTGTCTCCAGAAA
WI-19909a	29 T C ---	---	CCAGAAATAAGCCTGAATATTCCTTTCT/JCTTAAAAATAAATTTTCTCTTTGCTCTTCCAA GTAAATCTTAAATGAACCTGTTCTAGTCTATTTTAACTAGGCAATTATAACACTACCTAGCGGG TTTTTCTTTATACCTTGTTCTGTACTGTGGAATCACTAA
WI-20341	221 G C ---	---	TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAGTCTTAGGGGATGAGACATTAGGAAG GCCACAAATTATGAGTAATGAATGTGAGGCTGATGAGAAGCTACTGCTCCCATTTGTTAGCAGGA GGCAGGAAAAGTGATCTGGGGTCTCTGGCAGCAAAAGCGTGTGTAATATTTGGGTGACGTCATGC ATCCCCCATGCATTGGTTT/GJATGTCTCCAGTGAGCTGTTGGCAAGTCT

WI-20113	60	T C	---			TTCGGTACATGGTAAGTGCCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATACTGT[C]GGA AACAGTAAAGCAAAATACACACAATTAGGAGGAATATTTTCAGACATAGGATATTTAAACAT CACTCAAAATACTGGAGCATGATTACAGCAATAAATCTATCTCCATAAACAGGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTTCATGGATTCCGTATT
WI-20895	107	G C	---			TGATGGCAAGTACAAAGGCTCTGAAAGAACAGAGTAACAAGAGCAGCGCAGTGCAGCGTGTGGC CACTCCCACCGAGGAGAACACTTGACTTCAATTAAGGCAAA[G/C]CTTTACTCTGTTACTTTTCCTC CCACATAGTTTAACCCAAATAGAAAGGCATTCTATCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGGCAACAGATGCA
WI-20721	72	T C	---			CCTGCAATCACAAAAGTGGAACTAGTTGATATTTTGAATCATACTTGATTAAACCACCTTCAGAAA TTCTAT[C]IAAAACACTAGCAACTTCCTTTATCAGA
WI-19415c	161	A G	---			CTGGATTTTAATATTTCTGGCCTAATAACCAATGTAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTTCGAAGATTCCTTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAAA GTCAATGAGACCTTAGCTGATCTCAT[G]AAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103	C T	---			GCTGCTACTGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGCCATGCACCTTCG GCGTGCATGAAGAGACTGTTGGTCATGGCGTGA[C/T]GTCCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTGCTGCTGTAGAAAGCTTCTCC
WI-19348b	98	G A	---			GCTGCTACTGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGCCATGCACCTTCG GCGTGCATGAAGAGACTGTTGGTCATGGC[G/A]GTGACGCTCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTGCTGCTGTAGAAAGCTTCTCC
WI-19635	98	A T	---			ATTAGTTCGTGTGGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAACACAATG TTAAAGGTACAGTAAATAACAGTATTATATCTTATTGTAGCACGGCTGTGAGGCTCATT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGTCTGAAAGAACTTTGCCTT T
WI-19641a	46	A G	---			TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAGIAGTATTATAGTCTCATGTTT TTAATTTATGAATAACGCTGATTCATTGATTTTGTATTTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAAATAAATGGATCAGAGTAGTAAGTCAAGAAATAAGTGCATAATGTGGTTTAAATTTAAAA AATACTCAGAAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCACCTTG
WI-19642b	52	C A	---			ATATAGATACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCT[C/A]GGGTAAACCAG GACTATTGCATGAGCATCTTTAATACGTATTTTGTAGGACACAAGTTTCATGCTATTA
WI-19673b	180	C T	---			TCTGCCATGATCACATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACTTCTGTGTCATTGCCT TACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCACTGTAAATCTAATAGT GAAAAGGCAATGATGCTCAGTATCACTGTGAAAACATTTTTC[C/T]CTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCAAAAAACACAGCCC



WI-19673a	35	G A	---			TCTGCCATGATCACATTGTGATGAAGAACATGATG[A]TCACTAGTAGGTAACCTTCTGTGTCAATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCACCTGTAAATCTAAT AGTGAAGGCAATGATGCTCAGTATCACTGTGAACAACTTTTCCCTTGGACACGCTGAAGAA TCTTGAGGAGCCTGAAGCTTCAAGGTCCACACGTCACAAAACACAGCCC
WI-19724	35	A G	---			TTTATTTGGGAACAAAGGATTGTAATTTGGGTAA[A]GCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTGGTTTCTCTT
WI-19307	196	T C	---			TCCTCTCCCCAACTAGATGGTATTGATCACTCTGCCCCACAAATGGTACCCCCCTTCAGCAAGAACTG CAAGCCCTTCTGGATTGCTTCATGAGAAATGGTGGCTTGGGATGGAGGTGACATTCCTTGTCTGT GGTAACTGCAAGAAAGAACACAGGCAATGATTCATAGAGGCCCTTAAAGAGACCCG[T/C]TGG AATGGGCCATGGTCTAATTTGGTGTGAATAACTAACCTCTTTGGCTG
WI-19269	85	A T	---			CTTCCCTCATCCCTCTCCACACACCATCCGGAAGTGTCTCCAGGATTCCTGCCACTGGC CATTTGGAGTGTGCC[A/T]TTGGGTAGCAATGTGGAACACACAGGCCCTTTGGGAGAAATGG AGGGGTTGAGGGAGTCCAGGAGGGCTTATTGAGGGCTTTGCCACTTGTCTCATAGGGGAGCTCG ATCTCTCATCATCTGGACAGGTGGAAGCGAATCTTCCGGGGTAGGCA
WI-19946	122	C T	---			CAATGGACTGAATGAGTGGTGGTGGGGTGGGCGACACACACCTTCAATACAGTCAAGGTG CTTCCAGTTTGAAGAACAGAAATCTGCATCTCAGCCTGAGACGACAGAGAGGT[C/T]TCTCCTG ACCCAGACGCACTCAGAGCCAGGCTCTGGTTTCAAACTGCATTTAACTGCGCCAGAGAGTTTCA CGTAGGCATCTTTAATAACTAATCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	G A	---			CACAGCATGGTGAATAGCATCAGATTGAATGAAAGTTTAAATGCAACCATAAATAATTATA ATAAATATACATCAAGTAACCTTACAGCACACATTTTATGGGCCAAGGTTGGATCTGTGGACCT CAATGT[G/A]CTCTCGGAGAAAGCAGCAGCTTAGCAGCAGATACCTTACAGCTTGTCTACTCAA GTGATGGCCAAACAGAGCTTCTGAATCTCTCTCTGGGAGGTAGCTGACAAG
WI-19076	40	G A	---			TTGGTTGGATCTTCTGCTGGAAGAAAAAGAGCTTTAAI[G/A]GTATTCAAAATACCTTTAAAAA GTATCTAGCACAGATTTTCTGTAACTAGATTATGTTGTAACTTTTCTAAATCTTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCTTATCCAAATCTATCTTGGCTCTGAAAAACTGCAGA AAGGCACCTGAAAGCTGTTCTTAAGATATGGGATTCTTTTATCTT
WI-20218	26	T C	---			CCACACACTCTGGTTTATAAGCTA[T/C]AGGACAGAGCAGAGATGGAAGTGAACACAGGGTAG AAAAAACAATAAATGGAGGGGAACAGTGGGATGCAGAAAGATGACACAGCCACATGTGCCCCA GTCAAATACTTTTAGTCCCTGCAGCAGAAAGATGCCAACAGTCTCTATACTGGCTGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154	T G	---			CAACCTTTTGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATCATAATTG GGAATCTCTCTTTTAAATCTCCAGGCTTGATTGGGAGGGGCTGAGCTACCCCTTCTCTTCCCA TCCAGTCTATTGCCAGAT[G/C]CAGAGAAAGCGGGGAAGCCAGCTCTCCAGCATAGCCACTGTGG GTCCGGCTTCACTCTGTCTGACTCTCTCATGCTGGGACTTGTCTTTCGGG

WI-20361a	192	G A ---	---	CTGGAGTGTGACCTAAGTGACATTTTATGCAATACAGTAATCTCCAAGCTTTTAAATGGCTTATGCAAGATGACAGAATATGTGAATCTGATGTCGCCAGAGTTACACTCTGCACCTCCAAAGCTAACACAGTGCCACAGCTGAGAGTTTCCCTATATCTCTACTACTGTGACAAATTAGC[G/A]ATCCTTCAAATGGGAAATTCCTAACTACACGAGACAATGGTCTCTACAGTAGGCCCG
WI-20572	75	A G ---	---	GAGCCAAACCCAAACAAAATAAAACAGAACTCTTTTGTAAACTAAGTCATACCTACTTTCTTCTTCAGAAAT[G/G]TCATAAAACATCATCTTTTACAACATGGAGAAGCGAGGTAGGCCATAATTGTTCAATTCATCTTTCTCAAAATTTTAAATGTTTAAATCCCAAGGTGCCTATTGAATCTTCAAAAATAAATGCCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTGATTAT
WI-20588	133	G A ---	---	CATGACAAAGACAAAGATCAAGGAGTAACATAAATTATAAGTTGAATAAATAGTATACAGCAATCTTACATTTTAAAGAAATGTGAGATCCTTTGTTGGTTTTTATTTCCTTAAGTACAAAATGCTAAAC[G/A]GGAGCCGAGCTCTCCGCAATCAGG
WI-20593	79	A G ---	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTTGCTGACTTCAG[G/G]TTTAAATCTGGGAATGAGCATGCAATGCTCCACCAGATGAGGAAGAAAGCTGTTAAAGGAACCTCAGGATGTTGTTAGGAAGGGGAGTGATGCCAGGCTTCACCAGACTATCCAGAAGCCATTCATGGGGTATTTGGTCTGCATACTGTGAGACACTGAGCT
WI-19765	57	T C ---	---	TTCTTTGCCAAGCCTGTTCTCAAGTTATTCAGAACTGGGTGTATACCTTGTCCTCA[T/C]ATGTATCTTGTCCTGCTGCTTTTAGTTAGCAAGGTGTATGAATACTTTTAAAGTTTGTGTTCTTTTCCCTCGTGGTATCAGTGAATACTGATCTATTCTCTGGCTAGGGTCAATTTACAAAATTTGCCATGGAACTGAGC
WI-19066f	239	A G ---	---	AAAAGCCCCACGTGGGATAAAATCACTCACCATCGAGCGCCACCAGTATTTGACAAGGGGAGAGAGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC
WI-19066g	184	C T ---	---	AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATTC[CT]GGATGCTCAATTACAGTACCATGCAGGCAACCTTTTCTTAAACGCCCTTCACTA[G/G]TTTCTTTTAA
WI-19066h	148	T C ---	---	TGACAAGGGGAGAGAGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC
				AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATTC[CT]GGATGCTCAATTACAGTACCATGCAGGCAACCTTTTCTTAAACGCCCTTCACTA[G/G]TTTCTTTTAA
				TGACAAGGGGAGAGAGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC
				AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATTC[CT]GGATGCTCAATTACAGTACCATGCAGGCAACCTTTTCTTAAACGCCCTTCACTA[G/G]TTTCTTTTAA
				TGACAAGGGGAGAGAGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC
				AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATTC[CT]GGATGCTCAATTACAGTACCATGCAGGCAACCTTTTCTTAAACGCCCTTCACTA[G/G]TTTCTTTTAA
				TGACAAGGGGAGAGAGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC
				AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATTC[CT]GGATGCTCAATTACAGTACCATGCAGGCAACCTTTTCTTAAACGCCCTTCACTA[G/G]TTTCTTTTAA
				TGACAAGGGGAGAGAGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC
				AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATTC[CT]GGATGCTCAATTACAGTACCATGCAGGCAACCTTTTCTTAAACGCCCTTCACTA[G/G]TTTCTTTTAA

WI-19066	147	GC	---			TGACAGGGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTAGCCAGTCCAACTCTCTACGAGGAAC CATATGTTCTGC[G/C]TTGGTCAACCTGTAGCTGAATTAATCTCCATAATCCGGATGCTCAATTAC AGTACCAATTGACGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066c	100	GA	---			TGACAGGGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATC[G/A]TCTTAGCCAGTCCAACTCTCTACGAGGAAC TGGCATAATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCCATAATCCGGATGCTCAATTAC AGTACCAATTGACGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066b	87	CT	---			TGACAGGGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGA[G/C]TCTTCAAGCTGATCGTCTTAGCCAGTCCAACTCTCTACGAGGAAC TGGCATAATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCCATAATCCGGATGCTCAATTAC AGTACCAATTGACGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066a	72	CT	---			TGACAGGGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA[G/T]TTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAACTCTCTACGAGGAAC TGGCATAATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCCATAATCCGGATGCTCAATTAC AGTACCAATTGACGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-20660	105	GC	---			TTTACAGCGAGTTTTCCCGTCTCAATAAGTATGAATTAATAGATTAGGGTGAAGAAATGTG TGCTAAATAAAATCTCCCTTTTGAATGTATATTGT[G/C]TTATAAAGGGAAGCATTTAATATTA CAGACATAATTTACAAGGTTCTGAACATGAGTGAATCCATTACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCGCCGCCCAAAAATACTGTTTAAACAACACTATGTTTTAAGA CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGCGGTCTCTGCGAGCCTCCCTCAGTCTTCC TCCACCCGCCCTTCTTCCAGCCTGCCTGCATGCATGTGCACCCCTTGGT[C/T]TCGCTCCATCGCC TTGAAAGCTCTGAA
WI-18768	120	CT	---			TTCCCCAGGGTTCTGTATTGCAGTAAGCTCAATGTATTAATTAAGTCTAGTTGCTCTGCTTTG GTCCTCTTCCCAATGATGCTTACTACAGAAAGCAATCAGACACAATTAGAGAAGCCTTTTCCATAAA GTGTAATTTTAATGGCTGCAAAACCGCAACCTGTAACTGCCCTTTAAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-18790	49	AT	---			GAAAGCCAGAGATTAGCCCCGCTTCCGATCTGTCAACAGGACAGAAATJGATGGACAAAGGGA TGAGCTTTACAAAGATGATGCATTTGGAGATCAGAAAAATTCATATTTAAGCAAAAGTGATACAAACA CAGTGATTTGGGAATGCCT
WI-18987	35	GA	---			AGGAGGCTGTTCAGGAGTCTGCCCCAGCAGCCTC[G/A]GTGGCCAGCCCAGACACTACCCACCTT CCCCAGTGGCCCCGTGGATCTGGTCTAGGCTGGACACAGGATTCAGAAAGACACCAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTCAACAGCCCCCTACACTCAAGGCTGAGAGGCCCTCAGGAA AGTCA

WI-18919	26 C T ---			TGGATGAAACACAGGGATTCCGGAC/TGGCCAGACCCCATTTTACTTCACITTTCTCTACAGTG TTGTTTGTGTGTGTTTATTTTATCTTTGGCCATACACAGAGCTAGATTGCCCAGGTCT GGGCTGAATAAA
WI-18741c	64 G A ---			CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAAITTTACAAGCCCTGGATGAGGCTACTGA
WI-18741b	38 G C ---			CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCA[G/C]ACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATGCAAGTTAAITTTACAAGCCCTGGATGAGGCTACTGA
WI-18741a	23 T G ---			CTTCTGGTCAAGGCTTTGGACAT/GTCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATGCAAGTTAAITTTACAAGCCCTGGATGAGGCTACTGA
WI-19179a	170 G A ---			TCAGAAGCAGACATGGCATCTGTTCCCTTGGCTTGTGTTGTTGTGTACCTTTACGAGACCTGAATT TTAGAAATGCCAGTCTGCCAGAGTGAGTGAGTGAATCTCTCTTTCAGGTAAAGATAGGCTATCTC AACACTGCTGAGTGATTATCAAAACATATCAACCA[G/A]TAGCAITTAACCCATTTTATTTCTGTCTCTT AGTGCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCGCATGCT
WI-19212	46 T A ---			CCAAAGTGCATCCATGTTTGAITTTCTGATGAGACTAGAGTGACAGT[A/G]TTTCAGAACCCCAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTATGCAGATGGCCTATGGAATGAGCTGC ATAATTACACATTATCAAAGTCTCTTACAAITTTATTTCCGCAGCATGTCAGCTAAGTAGACCCA ATGGGAGAGAAATGCCTGCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210 G C ---			CTGTTGAAGGCTTCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAAGCACACATTGGATG GCAGCATGGGTTCTTCCCATTTATGGCATGAATATGTGTTTAGAATAAGGAACAAGCATTATT CCTTTGCCAACACAGCCTCACTTAAGAGGCTTTTGTGAGTCAAGCAACACTTGCCTGCTCTGCC CTTGGAG[G/C]TGCAITTTGACCTGCTCTCACTGGTAAAGGTGACTTGGTGGC
WI-20014b	214 T C ---			TTGAAATCCCAGTCTCTGCCCCCAGGCGGGTCTGTCAACCATAGATGTCTTCTCTACTGGGGTC GTTCTGGCTTTTGTAGAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAAGAGCAATGTTTCTGTATTCTGAACTGGAACTGAACCATTTGCCCTTCTCTAGTCACC AAGCATACTT[C/T]CCTGGCTCCCCAAGTACTTAAITGTTCTCATCTGT
WI-19041	198 T C ---			GTCTCCCCAGAGTGTCTTGCACCCAGCCCTGTCTGCTGTGAAGGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCAGGGGGTCCCTTAGTTTGGACATGCTGGTAGCAGGACTCCAGGGCGTG CACGGTAGCAGATGAGGCCCAAGCTCATCACACAGGGGGCCATCTTCTCAATACAGCC[T/C]G CCCTTGCAAGTCCCTATTTCAAAATAAAATTAGTGTGCTCTTGCCTGTCTGT
WI-19135	20 G A ---			CAGTTACCTGCTTTGCCCT[G/A]AAAGTGTCAATCAITTTGTATTTAGTATTAACTGTGAAAAGT GTCTGTAGGTAGTGTATTATATAGGACAGACCAAAATCAACCTATCAAAGCTTCAAAAAC TTGGGAAAGGGTGGATTAGTACAAAGCACATTTGGCTACAGTAAATGAAGTATTTTATTAACT GCTTTTGCCCATATAAAATGCTGATATTACTGTGAAACCTAGCCAGCTTCAAC

WI-19236	54	G A ---	---	TACACAGAGGGTGCACCTTGGACTCTGAGGGTGGGTGGAGGGGAAAGG(G/A)GATGGAGAC CTGCTCCCCAGCTCTCTCTGTACAGCGGTTTACATGGGAACAGGGTTAAGATCTGTGTAGGGAGGT CACCTTACCCTTTTTCATAGGGGAAGAGTGTACACTCTGGCTATCTCAGGGGAATGGGAAAG AATCTTTCAAGGGCAAGAACTCGTGGAGGATGTCTGTGTATGTAATACT
WI-19144	222	G C ---	---	GTGCCAGTCTTCAGAAAGCAAGGACTGCCCTTATTCAGCCTTCTGACCTCCAGCCTTTCTAAGG CTCAGCCCCACGGGACTCTGGTGGCTGCCAGCTTGTGAGCTATCTATCTATATTCATTTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACAGGAGGCTGTAGCCAGGAACCCCTCTCTTCCCTGGT CTGGCTCTGCTGGAGCGG(G/C)TGGGAACCAACACCTTCAGTCTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACAGAGGGTAGAC GGCAGATGCCCTGACAGAGAGTGGTTGGCAGACAACACACTAG(C/A)ATTTTCACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGCAGCATGTGGCGTCTCTGTGTGAAGCCACCGTGTCTCTTTGG GGGGCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTCGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACAGAGGGTAGA CTJGGCAGATGCCCTGACAGAGAGTGGTTGGCAGACAACACACTAGCATTTTCACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGCAGCATGTGGCGTCTCTGTGTGAAGCCACCGTGTCTCTTTGG GGGGCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTCGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGACCTTTAGGAAAGTGAATGCAGGTGAGAGAACCTAAACATGAAGGAAAGGGGTGCCT CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGTGT/CJGGCTCATGGCAGAGCAIT CAGTCCACCGTTTAGG
WI-19235	173	A G ---	---	TTCAGGAGGTGGAGTTCTGTCAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCTCTTCACTGCCCGAGTATGCTCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTTGTTCAACAATGGTGGAA(A/G)GCTTCATGTATATGATCAGGACCCACC TCCAGTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTTCTGCAGCACTA
WI-19222	179	C T ---	---	CGTTTCCCTAACTACCCAGTTAGTTGGGATGATTTGATTTCTGTGTGTGATCCCATTTCTAA CTTGGAAATTGTAGGCTCTATGTTTTCTGTAGGTGAGTGTGGGTTTTTCCCCCACCAGGAAGT GGCAGCATCCCTCCTTCCCTAAAGGACTCTGCGGAAC(C/T)TTTCACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGTGACACTGACGTGTCCAGAAGCAGCACTT
WI-19117	134	A G ---	---	AAATAATGCAACGCGAGGAGGAGAAAGAAATGCACTAAGACAAGAACATTTCTCTCATAGAACATTG ATCTGTTTTACAGGAACAAACCTTGCCTTGAAATTTACACAGTGAGACTGTACATAATTGCATGAA A(A/G)TAGCTATTTTTTCCCTAAGACATTTTTCATTCATGAATATTTCAAGTTTTTCATACTGTACA CATTCTTAAACACATGATACCAGCAGCACTGAAATGAATGCCGAATTG

WI-19134c	263 C T ---	---	---	CTCCTGTTGTCGACCTGACAGGGTGACACAGGCCCCCTTTCACACTCTGTCTCCTCCTCTCCTGGGTAGA TGCCCTGGTGTAGGGCTAGTACTGAATGGTCTCCATCCCGAGCAAGGGGTGCAGCCCGAGGGTGCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACATATCCTTTTCAGAGCAC TTCAATCCACTTGTCTCCTCCTACCTCGGCACCCCTGGGTGGGAAAGGG
WI-19134a	162 T C ---	---	---	CTCCTGTTGTCGACCTGACAGGGTGACACAGGCCCCCTTTCACACTCTGTCTCCTCCTCTCCTGGGTAGA TGCCCTGGTGTAGGGCTAGTACTGAATGGTCTCCATCCCGAGCAAGGGGTGCAGCCCGAGGGTGCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACATATCCTTTTCAGAG CACTTCATCCACTTGTCTCCTCCTACCTCGGCACCCCTGGGTGGGAA
WI-19224	112 C T ---	---	---	GGTTTCACAGTCTTTCAGGGAATCCGATGAAGTGTCCACAAAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACACAGAGGAGATAATCTCTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTTTATATCCAGCGGCCAGAAAGACTTCC AGGGAACTCATTCAAGGAGGTGAAAATGATGGATGACTCCTCCAAGATGAAAA
WI-19201	179 T C ---	---	---	GCAGCTCCTAAGGACCACCTGGCCATTAGCTCTTGCTTTTGATGGCATTCTCTTTCACCTTGCTTCTC CTTTGCTCCTCTGTGTAGTGTGGCAGGATGACAACTCATCCAGTGGAAACACAGCCTCAGACTGCC CTTCGCCCCCCACACTTTCGCTGCAGGTGCACCGAAAGGACCTCTGGGGGATAAAAATTCAAAAA GTGTGATGTGCTGCTCAGAAAGGTGAGACTCCTATGTCTGCTTGGCCTCAA
WI-19034	45 T C ---	---	---	GAAATGGCTCCACTCAGAGCTACCCGGTGTAGGATAGGGGAATCTCAGTCTTATTACATTAAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGCTGTTTGAAGTGAATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTTGATATACACTCAGCATTAAAGTTCTGTGCGAATTGAC ATTTGCTACTTATAAACTTAGTCCCTAAGTCTTCTATGCTGCTATATA
WI-19102	25 C G ---	---	---	TGTTCTGAGTCAAGCTGAGGAGAGCTGCTTCACTCAGGAGTTCATGCTGAGATCATGAGTTCA TGCGAGGTATATTTCTTTTGGAAACAGAAATGAAGCAGAGGAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAGAAGTCTAGAACTCCTGTAAAGTTTGAAGTCAAGGAGAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65 A G ---	---	---	AAAGGAGGGAGAAATCTTTTACATAAATGCCTTGATCATCCTCCAGTCCCTCACTGGGGAA[A/ G]AAAAAGCATCTNTCAAGTCTTTGTCACACTTTGGCTGC
WI-18548a	62 G A ---	---	---	AAAGGAGGGAGAAATCTTTTACATAAATGCCTTGATCATCCTCCAGTCCCTCACTGGGG[G/A] AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97 T C ---	---	---	GGCAGCAGCTTTTTTAAATTTGAACACTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTTTCJAAGATCCACAAATGCAAGGCCACTGCTGGCTCA CTCCTCACA
WI-18501	121 C T ---	---	---	CAGAGGGAAAGTTTATTGAGTCAGCCACAGAGGAACAGAAACACACAGAGGGTTCGTGT GCATGGAGGAAATCAGGGCGGNACAGCTGAACCTCGGCAGGACAGAGGGGGCTCTGGACAGCA GGCATGCCACAAACATTCA

WI-18017	87 C A ---			ACAAAGAAAATGGAATAGGTTGCGAAAACCTTATCTGCATGTACAAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA/C/AJACTGCTGGATAAATCGTTTATTAAATATATCTCTTTGCAT CAGAGCTGGTGGAAAATCAT
WI-18148b	101 A G ---			TTATTGGTTCCTTCGATAACCTCTCTTTGGGACTATGAGATCATACCAGATGTGAAAACGAAAGCA GTGATTTTCAGAAACNCGATCTGAATATCCC/A/GJTGCGGCATATGCAAGGGAAGATGA
WI-18254	64 T C ---			TATACGGATCATGTATTGTGTGACCAACCATACCACAGTCAATTTGTAGAGCAGTTAAATCAC/T/C JGCCAAATCCCTCTTGCTTCCTTGATGTCAGTCCCTCTCCCAACCCCGAGNACTTGGCAACCTGTTT TCCGTTCTAGACATTT
WI-18265b	117 C A ---			CAAATGGGTGGAGTGAGTATAAAACGCATATTGAGAAACAAGACGGCCTTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG/C/AJGTTTTCAACCTTTTC CTGGGTGGTTTCTTCAG
WI-18295	40 C T ---			ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG/C/JTTGGGAAGTAAAGGTTGATTACT TCCTCTCCAAGGATGATATGTTAATGAATCCCTTNCCTTAGCTTCATTCTTCATAATGOCAAA
WI-18459b	64 T C ---			GGGCAAGAGACAGAGATTTAATTGAATAAACTCCAGGCTGTACACGGTGGGAGACACAA/T/ CJGAGTAATTAAACAACATAATTTTANATGACAGTGCAATTAATTAACGTCCTGGGTAAGCCAGAG GGGAGAGGGGCTCTTCA
WI-22585	56 A G ---			TTTATTTTAAATTTGCATCCTGAGATAATAAAATTTTATCTGACAAGTGAACAATG/A/GJCAGAAGC AGCAGTGAAAGTTTCGGAGAGGCGATGATCTTCAATTTTGGCACAGCTGTATATAGATTGA
WI-21155	36 A G ---			GGGCTGTGGAGTAACAGAACTTGATGGAAAATTTGGC/A/GJCTGTGTAGATGATCTTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88 G A ---			GCCTTTGCTCTTTGCTGCTCAGAGGCTCAGATGGATACGACAGCAACTTCTTTTGAACCTTTTAT TTTCTGGCAGGAAGAAG/AJGGATCCAGCAGTGAGATCAGGCAGGTTCTGTGTGCACAGACAG GGAAACAGGC
WI-19888a	98 C T ---			GGCACGATTCAACCCATAACAGAGAAATAACTCCTTATTGGAACAAGGTTTTTATTTGATATGATG AAAAATATTTGGAACTAGAAAGTAGCAGTGA/C/JTTGGACAACGTTGTAAAGATATTAAATGCCACT GAACTGTTTCATTTAAATGGTAATTTTCATGTATGTGTTTACCTCAATTAAGAATGGAACATGT CTTATAATTGTAATTTACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82 C T ---			TGAGACCATCCTCCTCAACAAGAATCAGTCAGTTTCAGCACCTAATTTTCCACACTGAAGTCTACG CAATTTTCATGCAG/C/JTTGTGCACACAGTACAGTGACAAATCCAGAGGGGCAACACATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125 T C ---			TCAGAAATGCTTTCCACTGCCCAACCAAGAAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCTTGGAGGTTGCATGACAGGATTAGTCTTCTGTGTT/CJCTTGGT GCAAGTTTGAACCAAGTATTAAGTACCATTTGCATGAGAGCATCTGTTTCCCTGTGAGATCCCACTAG

WI-20561b	94	T C ---	CGTTGCTTATTTAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATTATG TACTTCAGATGAAAAATCCTTACATGTC/G]GGAATCAATGTCTTTTAAAAATTCAGATAAAGAATTT NCAITTGAGGAGACATACAATTGTAA
WI-20561a	25	A G ---	CGTTGCTTATTTAAGATGGCTGTTT[A/G]TAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATTA TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAAAATTCAGATAAAGAATTT NCAITTGAGGAGACATACAATTGTAA
WI-20116e	69	T A ---	GCITTCATTTCTGTCACCCACCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT A/T/ATAAATCTATATCATATATTTATACACACAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATNGCACAGGTTTGCTCTATGCAA GAATTCACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCCGAGATAA
WI-20116c	59	T A ---	GCITTCATTTCTGTCACCCACCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGT/TA]TAGAA CATATATAAATCTATATCATATATTTATACACACAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATNGCACAGGTTTGCTCTATGCAA GAATTCACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCCGAGATAA
WI-20116a	22	C G ---	GCITTCATTTCTGTCACCCAC/C/G]CTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAAATCTATATCATATATTTATACACACAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATNGCACAGGTTTGCTCTATGCAA GAATTCACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCCGAGATAA
WI-20466b	133	G A ---	AAAGATTGCAGTCTGGGACACAGTTTGGAAACACTATTTAAGTTGCACATATTACAAACAG NTCCAAATGGTGAACCTGGTATCTAAGATGAAGCTTAATGAACATAATGAAGTGAATAAACGC/ G/ATGTGAACATAATGTTTAAAAAGTTAGAGCTTGCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTGTCTTTTATCCCTTTCCAGGTTCCGATT
WI-21034b	39	A G ---	CTGGGCAGCAAGTAACCATTTTAAAGAAATACTCTCAAC/GIAGTCTTTTATGGGGTATTTCA GTTGTTAAACAAAGTTAAAAATACTTATTGGAACATACTTCTTGATTTATTCGAGGAAGAAGAATCT ATAAGATTGACTTACTCAATTGTTGACTGGTTTTTTGAAGCCTTACTGGGG
WI-21034b	148	T C ---	AGAATGGACAATGATGCAGATGTTTGTGAGCATTTTGTAGAAAGTGGTGATTAGAAGGATACAG CATAAATTTAAATGTAAACATGCTTATCTAGCTAACCTTAATCTGTTTCTGTAGAATTTACTGGTCATGG GAGATTGGATAGAT/C]GCCTAACCTATCTCAATTTTAAAGTAATGTGAGCAA
WI-22091c	205	G A ---	GGCGTGATTTTGATGCAATGTCCAACCAGTCAAGCTATCATTTGAATCCAAATATTTCCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAAGCATATTACCTCCCCCTTAAGTGACTCATAATTC ATTACTTGTGCTGTAGCTTTTAAAGGTTTAAAAATGTGTAGCATTAAAGTGTATTTACTTGAGGGCA ACA/G/A]AATTACGGCTTAACAACACACTAAATCATGAGGCTCAGGGGATTG



WI-21805a	45 A T ---	---	CAACTGCTGAGGCTCTTCACTAGCTGATTATTAATCCTATATTATJAAAAAAAAATCTATAGTCTG CAGTCTTTGACATACTTCTCAAGGGTGGATATGTGGGAATGCAGACTCCATCAATATGTGTGGTT TTGTTGCTTTTGTAGCTTAAGTCTGTTTGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTTCATAAAATCGAACAGTTGAAGGCTGTTTGTAAATTGCTG
WI-21778b	155 T C ---	---	AAAAATCCATAATATTGAACCCCAAGTTACAGAGAAAGTTCTGTAACCTTTTTTATTGAATTATTGAC TCTGCCCGGTGCTGTTGCTGCTTCAACTCCAGTCTGTAATGCCCTGTGTAGTGGGGTCCCCAG GTCTGGGCTTCTGAGGTCCT/CJGGTAGAAGGAGGCGAGTGGT
WI-20907	241 A C ---	---	TGAGTCAGTGGTCAGATGGGGCAGTTGCGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCCTCT CAAAATGATCTAGAGCTCATCTTGGGCGTACATGAGGGGCAGTTGTTGTTCTAGTACCCATTAGCCOC ATGGCTCTTCAAGCCCAATTCACACTGGGAAAAACACACCTCACAAGATGCCTATCCATTGAGTTTC ATACAGGTTTGTAGTAGCTAGAACTAAAAAACATTTTAA/CJAATTATCTA
WI-21449b	222 C T ---	---	AACAGCAGCAGTCACTTCCAAAAATGCAAAAAAATTAACAATTTTAGAATAAAATTATAATGTTTA TAATGCGGGTCAGAAGANTTGAAGGTACACAGAAATCAATCACGCAGCACTGGAGCGGCTGGAG AAGCCAAAGCCCACTGGTCAGGGGTCCAAGCTGACAAGAGTCCCACTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCA/CJTTCACAGAGCCAGTGTCTCTGGGTTAG
WI-21558a	157 G A ---	---	GCTTACAAGGAAGCCTGTGGACAGCGAGNTGGGTGGAACCGACTCCAGCTCGAAACCTGCCCTC CCATCCCTTAGCGCTTCTTGGCTTCCGGCTGATTTCTTCGACAGCAGTTCTGGCCAGGGCAAGG AGCTGTGGTGGGGGCGAGTATG/AJAGCCAGGGACTCCCTCCACAGATGAGGCTAGGGCTGCAA AAGGCCCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-22187b	178 G A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATGTTGGGGCCGTGGCTAGCAGAGCTCATGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAACCAAAACAAAAATACCAAGA ACAGATCACTTGGCATGGACATCAGTAATCTATTGGTAATGGTG/G/AJAAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAAACTGTCTCTTACCCCAAAAGTGTCTGGAGGAAAG
WI-22187a	110 C A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATGTTGGGGCCGTGGCTAGCAGAGCTCATGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAA/CJA)CAAAACAAAAATACCA AGAACAGATCACTTGGCATGGACATCAGTAATCTATTGGTAATGGTGGAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAAACTGTCTCTTACCCCAAAAGTGTCTGGAGGAAAG
WI-21609b	146 G A ---	---	TCATGAATATGCAGCCTCCATAATCTCTCCCTTGTAAACAAACGTGCAGTCCGTTTCAAGCTGTAAA AACAAGCCCAACCCCAAGACATCACAGAGGCAAGCAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTTCAAG/G/AJAGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	TCATGAATATGCAGCCTCCATAATCTTCCCTTGTAAACAAAC/CTGTGCAGTCCGTTCCACAAAGCTGT AAAAACAAGCCAAACCCCAAGACATCACAAAGAGGCAAGCAGTGGCAGTGAGAAAGGAGCCTGTGA AAGGATGTTTCAAAGGAGGGTCCCGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---	---	ACATTCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGGCCTCCCTAGGGCTTCA GGTAAGCCCTGACATCATGCTCTTTGTGATCTGT/CTACCTCACCCATGCTCCCCACCTNAGTTCC CACATTTCCCCACGICTAAGGCGAGGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	ATCGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTTAAAGGCTCA CAACACTAAAGATTTCACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGATATGTGACAGGG TTTC/AGTGTGCACTGGTACAGAAACACACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---	---	ATCGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTTAAAGGCTCA CAACACTAAAGATTTCACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGG/ATGTATGTGACAG GGTTTCATGCACTGGTACAGAAACACACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	ACAACATGCCTGTTACAGGGGGGAAAATCCTAGGNAATAACTTATGTGACTTCTTG/AGTTCATCA TCATACAAGACAAAGCACAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---	---	ACAACATGCCTGTTACAGGGGGGAAAATCCTAGGTT/AAATAACTTATGTGACTTCTTGATTTCA TCATACAAGACAAAGCACAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---	---	AGCCAACTCAAGGCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAGGA GCACAGGTAGTCCACAGAATA/AGACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAATACTAAGATTAGATGAACACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAAAGAAC AGATGTTAACAAAAACAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	CTCTGAACCTAAAGGCCGCTGAAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCAIT/AAACAT TGGCTGGAATGAGGTGGTCAGGAAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTCTGGAGAAAGTTAAAGTGTAAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCTTAGGT
WI- 22130b	165 C T ---	---	TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAAGGGCTGCCTTCCCTCTCCTGACAC CAGCAAGGGGGAGGCACCATCACCAGGCTGCCCCATCATGCATCAATGATTACTAGCACTAGGAA GCCAACGGAANAGGACCCCGCGCTTGTCT/CTGTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTCTGTGATGGGAATGAC

WI-21661	117 G C ---	---	GCTAGTCTCCACCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGTCTTCCAACTTTAGAAATGATAAATAAGAAATGACATTTTAAATAAAATAG/CJTTTAGTCACAGTCACACAAAACCTACTTAAGGAAAACCTGTCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAGGA
WI-21980a	25 T C ---	---	TCAGTTTAAACACACATTCATCAAGGAT/CJAGATTAAATATGTCAAGGTAGCATAAAAGGGAGATTATAAACAGAAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTAATTTTCATGGGTGAAGCCCTGGGATAAAG
WI-21636	71 A G ---	---	TGCTTGATTAATGTGGTGTTCACATTATCCTATTTCACAGATGGAACAGAAAATACACGCTTTTTTAAA[A/G]TAGCAATATCTATTATTATAATAAATTGAAAATAACACCAATAATAATATCATAAGGAAGTAATCTAATTGTGTTGATTTCAGAGGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGCTCATGCAAACTCAATCTGAAGGTGTAGAACTAGGAAGGACAGGGATTTC
WI-22457a	112 G A ---	---	TTGCTATAATTTCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAAATCACATCATTAGA CAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACA[G/A]CAGTTAAATTAACATAAAG GAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGAAACAGTAATGCAGTAAATACCTGGGCC AAAACCCACTGAACCTACCCAGCTGAAAACACTGAAGGATACCTGGGTAAAGGA
WI-21524b	97 C T ---	---	GCCGTGAGGGTAGCGTATAATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGCGTCATACCTTAT AATGGTTAATAACAGCATTCTCTGTACCC[C/TT]GATGATGCTTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCGACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCTCCAGGGGATG
WI-21524a	35 A C ---	---	GCCGTGAGGGTAGCGTATAATGAAAAGGTGTAAT/CJGCTGATGTACGACCTTCGCGTCATACCT TATAATGGTTAATAACAGCATTCTGTCTACCCGATGATGCTTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCGACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCTCCAGGGGATG
WI-22652a	32 G T ---	---	TTACCTTCCAAACCAAGGCCACTTTGGAGAAAG[G/TT]AAGAGAATGCTATTAAATCAATAAGCCAAGAC AATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACCATCATCTCTGCCACAGAACC TTGACATGCTGCCCTCCCTACTCCGCACTACCTGTCTAATTTGGGACCTGAAGCTTCAGCATCCCTT CTTTAGGG
WI-21703d	197 A G ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGACATAGGAGGTGGTGTGGGCGAGGGCTC TGCATCCCTTTCTCAGCAGACAGCACCCTTTCACCCCTCTGGGAAAGCAATTGGAGCCTACACCA CTTGTGCTTTTCTCACCAGGGTAAGAAATGCAGGATTTCAGAGGGGAGTGAGTCTGGGAA[A/G]G TGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG



WI-22724	117	A G ---	---	TGATATGATGTCTGAGATTTGCTTCCAAATATGCCTAGGAAGGGAAGTGTTTAGAGATATAGGA CAAATCAAGATTGTCAAATGTATAGTAAGTGTAAAGCTTGTAAAGGT[A/G]GTTATTCTATTTT TGGGATATGTTTGGGAATT
WI-22750	48	G A ---	---	TGTAACCTGTGTTTCCCTGAAAGTTGAGGAAAGCTGAGGCAGCTAAT[G/A]GGCTCATACAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTTCTGACCATTTCTGACTGTGCT
WI-2275a	60	A G ---	---	TGCTGTTCTTTAGTTCATGACGTTTATCACAATGTCGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGAATAAATCCCTAAGGCGAGCAATAATTTCTGTCTTTGAATCCTTCATTCAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAAGTGGGATGTTAGGTGTTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143	C T ---	---	CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAAGTCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAAGAGAGTAGGTATAAGAACCCAGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G A ---	---	TCTCTGTGTCTTGAGCCCTATCCCCACCCCTCCAAAGCCCTCATGCCAACACACCCGTGTCCACATT CCCCATCCTCCCTGTCTGCTCCCATCTCAAGTCCAAATCCAAAGGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGCATGAAAGGAGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGGCTGTGGGTC CTG[A/T]TGGCGTGGTATGTGGGGGCCAATCCTGAGGCCAGAGTTCA
WI-21031	31	C T ---	---	TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCCATTGTCTCCAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAAACACACACA
WI-21314	122	A T ---	---	CCATATCCAGTCTCTTTGAAGCTTTCTATTGACTTTTAGGGTTCAGTTATTATATCCTTTATCACTAT GACTTTCAATTTGATTTTTTATTGTTTCTCCATTCTCTGCAAACTTTTC[A/T]TTTGTATTATAA ACTGTTTCTAAACTTCACCTAATCTCTATCTGTATTNCTTGTAGTCCCTGAACCTCTTTTAGAGG
WI-21186	95	G A ---	---	AGCAGCATCAGAATCACCCTAGAGGGTTGACTAAACAGACTCTGGACCCAAACCCAGAGCTTCT GATTGAGTAGGCCTGAGGTGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCCTAAGTGTGCAG ATGCTGCTTGTCOCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCCTTTCTTTAAA GGAGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATAATGTATTGAAT
WI-21187a	94	A G ---	---	CCACGATAACTATAAAGCAGAAAAATTAGCTTTGAAAAATCAAATAACATATTTAGTAACACACATT CATTTTATAAACACACATAAAGACACC[A/G]GENTCTCAGTAATGCTCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCCATTTGCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39	T C	---			TTTTCCACATACCAATGCACCTGTTTGTATAAACTATTCGCTGGGGTAAGCCCTTCCTTTGGAGAC CAGTGACATAGACATGATCCCATATATTAACAAATATTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTATTGAGAAAGGAGAGTCAGCATAGTTTATTTCCATGTAATAAAAGCTT AACACA
WI-19937d	186	G A	---			ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCTCTCAGCAAGTCGATCCAAACCTTC CAAAAAGAGGAGTCATTGAAAAATGCTGACTTATGCATTGCTCAGGAAGAA
WI-19937c	185	C T	---			ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCTCTCAGCAAGTCGATCCAAACCTTC CAAAAAGAGGAGTCATTGAAAAATGCTGACTTATGCATTGCTCAGGAAGAA
WI-2117b	227	C T	---			GAAACGGGGTGCTAAACAAGAAAAGTCTCAGATCCCACTGAAAATCTGTTTCAGTTTCACAGGCTC TCTCCAGAAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAATACATCTCGGG TCCAATCACATACCTCAGGTTTCAGACTCTCAGTCCCAATATCTCAGAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGTATTTCCTACTGAATCTTGGTGGGAG
WI-21122a	42	C T	---			TCACITTTGATCATAATCCCTGTAAAAGCTAAAGTTATTCACATCTAACAGGAACTCTGTTTTCCTC TTATTCAATGTGCACAAGCCTGACGCTTACTGTACATATCTGACAGGAGACAACTGGAATACT AAACAAATACTGGAATTCACATTACAGACAGCAACCAACATGGGATGCCACACATAACTTCTCT TTGTAGGTTTCACAGAGAGCCTATTGTTGGTGTCT
WI-21254	53	A G	---			CAGTTTGTACAGGAAGGGCCCATGAATGTGGGCGGAACCTATCCACAGGAGATGCAAGGAGAAG CTGTTCTCTGG
WI-21054	23	G T	---			AAGGAACTGCATGGGTACAAATGTTTCCAATTCATACTTAACAAGGTGGGAAACGGGTCATTCT TGGCTGCTCCAGAACCAAGGGGCGAGTCTATGCACCTCTG
WI-21059b	181	T C	---			GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTCCTGGCTTGCATTTCCAGCTTCGTCACATCTTAATTTCAAGCTGAAA AATCCTGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCGATTTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63	C T	---			GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCACTGAGCCTGGCTGTT GAACTACAGCTGCCAGCATTCCTGGCTTGCATTTCCAGCTTCGTCACATCTTAATTTCAAGCTG AAAAATCCTGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT

WI-20442	37	T C	---				TCCACGTTGAAGGAAGAAAAAANGGGGGGGCTT/CJTAAAGTGGCACAATTTTAAAGAAAT ACCATCCATTTTTCAGTCTAATCTGAATCCATACATTAAACAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43	T C	---				GTGACAAGAGGTGAAGCAAGGACAAGGGGCAGCAGGGCAGTCT/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	T C	---				ATCAGAACTGCAATCTGCACATGAAAGACCTGGGGGAATGCCTACATCTGGAATTT/CJCATTA ATCAACGTTAAATTTTGTCGACCAAGTCTTCATTGCTGATCACTTTTGATAATGACAGATCCAACAT GAAACTCCTGAAGCAAAATGAATATTTACCTTTGCTTTTCATGCAAAATTTAGGGACCAAACTCAAGG TTTCATCCATGCTGGGACACCAGATCTAAGGAATTTGTACAGGGATCTTCT
WI-21149a	167	G A	---				AGGACCTGCTCTCACAGTTCCCTCACCCACCAGCTTTTGGCAAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTTTTTTTTTAAACATGACCTTATTTATCTTTTAACTTTAACTGAGTCTTATATA CAGACCTGCCAACTGGAAGCTTTTACAC/GATGCTTCAGAAATCGGCAGTATTCACAAATGGTT TGGGGCAGGTTCTGTGTTAAACATGGGATGGAACCCAGGCTACCTG
WI-21376b	188	A G	---				GGTGTCAACTTGGAAATAATGGTTTAAAAACAGGATAAGCATTAAGAAAAACACTTCAATGTGTC TTCCATTTGATGAATTTGTTTTCTCTCTTATCCCGCAAGTGGAGTTTCATGCTCGGTGAAACCA GACAGTGTGAATCTGTTCCAGGCCAAATCTGCAGCATTAGGGATGAGTTCTC/A/GJGAAGTGATTCT GAACTGAGCAGCACTCATGTCTGCATGGGGAACCTCTGGGAGAGAAGCCT
WI-21382d	125	C G	---				CCATTGCAGTCCAGAGATGAGAAACTGGACCAGAGGCAATCATGAACAGACGGGAGTCAAGAGA AGGGTTTCTAAGATGGAGAAGTGGGGGGGTTTGGATCCAGTGGGATNTGGCTTCC/CJGAGGTT GCAACCCAAAGGAGTCTGTGGAAGCAGCACCAGTCTGATGGGGAGCAGAAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAGGGTCCGAGGAGAGCTGCTCTCCATAGTCTGCGAC
WI-21437a	201	G A	---				TCCCTGAGGTTGGAGTCTAGCATAGCTCCCTCCCTCAAGAGGACAAAGGGGTGAGGGCAGAGC AAAAATCCAGTCTGTTCAACCACGGAGACTGCCCTTTGGGATGGAAGTTTCTGGAGCTCCCTCCATT CTATTCTGTGGGGCAGGAACATGCCAGGGCTGCTGGTAAATGCGAGGGTCACTTTTACCAGGGC/G /AJCAGGCATAGTGTGGCCCTGCTGCCCTGGGGGCCACCTTGGGAACAGT
WI-21202b	156	A C	---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAACTGATTTTATGAGGG AGGAGGAGAGAGTTGACCAA/A/CJGTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A
WI-21202a	61	T C	---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATGA TCTGTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAACTGATTTTATGAGG GGGAGGAGGAGAGTTGACCAAAGTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---			GCATGAAAGAACTCCAATCAGACITTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATATTGATATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAA[A/G]TCCAAAGTCATCTAATATTAACCATATTTACATAAATTTGTAGG GACGTATACTAATACTCTACAATAAAGGGTTTAAAAATGTGTGCTTA
WI-21627a	106 A G ---			GCATGAAAGAACTCCAATCAGACITTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTC[A/G]TTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATTAACCATATTTACATAAATTTGTAGG GACGTATACTAATACTCTACAATAAAGGGTTTAAAAATGTGTGCTTA
WI-21399a	75 C T ---			GGATTTGAGTCCCAACTGATCTCAAAATTCATCTTGATGTAAACAAGCTCATTCCTCTAAAGTT TCAGTTT[C/T]TCACCAGTAAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATGCTTGGTAA CTGCCCTCTGCAATTTGCTCTGAGGTTGTGTGTCCTAGGACTAGGATCTCTCTGCTTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATCTTGT
WI-20329a	68 G A ---			CGATGCTCTGAAGATAGGAGGTTAATTTTACATGGTGAGTGGTCACAGACAGACATCAAT C[G/A]TCTGTTAGCAGCGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTGTGGCTTCTTAAACACAGTAAACCAATCAAAAGAAAGATTAGAGGTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTGAAGGGAAAGGCCTCACT
WI-21249	155 T C ---			TTCTGGCATTCAAATGTACATGTAAATCCAAATTTAACAGATCAAAATTTGTACACTAAGTTTCACCT TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACITTTAAGAAACATTTAAGGTAATT AAACTCTAGGTGTACTATT[C/G]ATGGAACCTAGTTTATTCNATTTAACTACTGTTTCATTGGGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTAAAGGAATTAATAAACATTGAGA
WI-21504	147 C T ---			TGACACAGCATCAATTTTCATGAATACTTTGAAGGGCCATTAGAAAAAATAGAGCCCAATTTGGGTC ATTTGAGAAACATTTTCAGCACAATTACAGTGGGGGCACGGCCGTTCCGCTCCAGCTGGGTTTCCCC AGATGCAACAAT[C/G]GCGGTTCTGGCTTCTCCACTGGTGGGATGGGATCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---			CTGCACCAGGGAGGACAGCTGTGGCAGGGACTAATAAACCCCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAACCGCGGCGAGGGAGGGCAGAGAAC[G/A]CACTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT
WI-21475c	181 A G ---			TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGGACGTTGCCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGTGGGCTCCAAACCCAGGCTTCTCACTTCTTACTAAGCACAG CAGTCTGAAGCTTTGGGACCTGGGACGTGGCTCTTTTGAGAAAGGCA[A/G]AAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCCGTTCTCCACCCCTATTCTCCCTCCCTGAAG



WI-21475b	117 A T ---	---	TAGCCTTCTGCCAATCTGGCAATNTGAGGCTGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTC/A/TCTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGCAGTGGCTTTGGAGAAGGCAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTCCCGTCTCCACCTATTTCTCCCTCCCTGAAG
WI-20893d	207 A G ---	---	TGTTTGTTCCAGCCACATCTTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGTGCAGGG CTGCTTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTGTCAGTAACTCATCCGCACTCC AGCGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTTCTTCTTTTACAATGCAGT TTC/A/G/JACATAACATTGGTAGAGTAACAACAACCAAGCCTAAATG
WI-20893c	179 T C ---	---	TGTTTGTTCCAGCCACATCTTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGTGCAGGG CTGCTTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTGTCAGTAACTCATCCGCACTCC AGCGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCAT/CJTTCCTTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAACAACAACCAAGCCTAAATG
WI-19941c	71 C G ---	---	GAGCTCAAGGGAAGACCTTACCCAGATAGGGACTAAGTGGAGGGTGAAGGAACAAGGTGAAA GGTAT/C/G/JGGTCTGGTGAGACAAAAGCAGGGGGCTGAGAACACAGCAAGGTGGTTGGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGACATTTCTTATCCAGTGCATGTCCCTTAAAT AACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAACAAAGCG
WI-21552b	166 C A ---	---	TGGGTACATGGACAGATGATATGTTTATGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAATCGGATCTCTCACCTCAAGCATTTATCCATAGTTTACAAGAA TCCAAGTACTCTTGATTATTTAAAATGTACAAATTAATTTGAATTTAGTTACCCCA ATTGTCTATCAAAATTCATCTTATTCATCTTTGTAACCTATTTATTGTA
WI-21552a	66 G A ---	---	TGGGTACATGGACAGATGATATGTTTATGGTTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAATCGGATCTCTCACCTCAAGCATTTATCCATAGTTTACAAG AATCCAAGTACTCTTGATTATTTAAAATGTACAAATTAATTTGAATTTAGTTACCCCA TTGTGCTATCAAAATTCATCTTATTCATCTTTGTAACCTATTTATTGTA
WI-21512	54 C G ---	---	TCCTCGTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAATATTTCTGT/C/G/JTAGAGAGGA AAGAGCTGGTCCCTGCTGGAGGCAACGTCAGGTCGGGAAAGGCACTGGTGTCTGTGATCTGTC TCAGTGATGGAGGCTCCACTCGCCCCACAGGAGCCTCGGGCCAGAGATGAGAATATGCTGTAA TCCAGTACAGGGGCTGGTGGGTCCCAACAGCTCTCTTTGGGGG
WI-21513b	192 G A ---	---	CACATAGTTTCTCAAGAAAGAGGATGAACCTGAAAACCTCTTAAGGCAGGACAAAGCACTTTCCATT ATTCTTAGTTAGACCAGAACTTTAAATTTATATTCTCTTTAATAACTGTCAAAATACACCAATA CTTAGAGGAAAATATTCACAGTATACCAAAACATTTTAAGATAAAGGAGCGTGTAA/G/A/JAGTAG TATTCTCTACATACCACAGTATACAATGATGCCCTTCTGTCAGGTTTAGGAAC

WI-21514b	133 C T ---			TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAGGAGCACATTACCATGGAGC[C /T]ACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCCTTATGCAGGAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTATTGTCAAGGGTCATAAGGAACT
WI-21514a	100 A G ---			TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAAGTATCTCAACATTACAAAACCCCAAG/G]TCTTCAAGGAAGGAGCACATTACCATGGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCCTTATGCAGGAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTATTGTCAAGGGTCATAAGGAACT
WI-22020	27 C G ---			ATGAACATGTTGCAGTGGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATTTCTACCTGTATGAGGGTACTT
WI-19576a	113 A G ---			TTTCATCGGTTCTTAATACAGTACAATCCTTTTGTGAAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATT[C]A/G]TCTAGTTCAAGTATTAGT CACAGAAANTTAACATCTGCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGGA G
WI-21695a	141 A C ---			ATACAGAGGCCACAATTGCAGGATGGAAGGAGGCGACTGGGCACCTTGGAAAGTGAATGACTACACATGGCAATA AGCAGCCTATCTCTTTACCAACAGAAAGTTCTTGGGGCATGTGATGGTAGCCAGACCCCTTTCCAA GGGAAT[A/C]TACTACACTAAGCCTACACTGTACTGTGAGAGTCATGTGGTGAACAAGGCCACAGGC AGTGGGAGGAAATGTGATGACTTCACTGTGTTTCAGANTTCTAAGGCCACAGCAT
WI-21574a	235 C T ---			AAACCCAGAAATTTAGGTACTTTTGTATTATGAGGAATCACTATACTAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTTCCACTGATCTGGAGGTGACAGCTCTCAGTGAACAGCGC TCATCACTAAAGTGAGAGGCTGTCTATTCTCAITTTGTAATGTCCCTCAGAGTCACTAGGGAGCCATT GGGCAGGCCAGGGAACCTTACTGCCTACTTCTCTCTGTCAGGTGGGA
WI-21644c	151 T A ---			TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGGTCACCTTAACCTTTACAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTACCANTANTTTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGA[T/A]TTCATCAAGATCCATGGAATGATGCAGTTTAACATGTGTCTCAGC TTGCCTACTGACCACTTCTCTTTCTAAATATGGCAACAGCACAGCAAGTC
WI-21614b	55 G A ---			TGTCCTTTAACCTCAAAAGTCCAAATAAACATATAGACATTTTANTATAGCTATC[G/A]TTTTAACA AACCTCATTTATGATCACTGTGCAATTTTCAGTCACCTAAATACGGAACCACTGACTATTAAATAACA TTTACTGTGTGGGTTTGTGGGACTGAACATAAACCATACGTGTATTCTTAAGGTACTAGGGAGTT GGAAACAGCTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI-21615b	151 C T ---			GACCGAAAAAACTGCAAGGCATATGATGTTTGTGCAAGTATCACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTTACATATTAAGATAAGGATGGACT CTTTCACCTGAGTATTAT[C/T]AGGACACAATCGACGGATGTAATCTATTTGANTTATACCATAGGCC TATTCTATTTGGCCAAAGGGAAGGTAGGATGGGTACTGIGGAAACGGA

WI-21981	61 T A ---	---	TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATAATTCTTGAAGAAAAAAAT/AJGT CTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAGTACATGACAACATGCATGGGATAGA CACTCTGTTCTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGAGGCGTTTAAAGTTAAATTTGG
WI-21660	120 C T ---	---	TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAAACACGCCCTCTCCACTGCT TACTGTGTACCAAGAGGAGGAGGAGGAGCTACCCAAAGCCTAACCTGGCC/TTJGTCTTTTCAG GCTTCTCAGGATGCCACAGCACATACCTGAGGAACTGGGATGCAGGGGAGAACCCAGGGTCTGTCTTC AGGAGGGTCACAGC
WI-19105c	211 C T ---	---	TGGAAGTAGCCCTTCTGGACAGAAAGAATATTTGTGGTCCATGTGGTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGTGGAACTCCTCCTT GTCTGATGTTTCCAGGGCTGGCCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGGATCTCCTC ACAACTTC/TTCCAGGGGAGGATTTCCACCCAGGGGCCAGGGTGCCCG
WI-19105a	33 T C ---	---	TGGAAGTAGCCCTTCTGGACAGAAAGAATATTT/CJGTGGTCCATGTGGTTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGTGGAACTCCTC CTTGCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGGATCTC CCACAACTTCTCTCAGGGGAGGATTTCCACCCAGGGGCCAGGGTGCCCG
WI-21760c	81 C A ---	---	CAAACTTAGTCACTACTGATGCAAAATGATTGGAGGTGTTCTCTAGCTTTACAATAAGNGGAGG GACCTCTGACTGCA/C/AJCCCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	CAAACTTAGTCACTACTGATGCAAAATGATTGGAGGTGTTCTCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCACCCCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	TCTGCCATATTGTTCCAGCACTACTTACTGTTATTATTTCTCTTTGAGGAAACCAGGNATTAAG AAATCTGGTTTGAATTTCCATGATGCCCTAACTCTATGGTTAAAATCCTTTTCCTTACCAAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTGCAGAAATTTATCTCTAC/T/CJ AGAGACAATTCATAGTTTCATAATCTTTCAGGGTTGTGCTTTACTTGGGGGGC
WI-20934a	72 T G ---	---	CCAACATGCAACATAGTCTTCATTTCTTAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCA GAGAA/TJGTCTAAGACAAATGGTCAAAATATTCAATGGCTGGCACTAGTGGTAATTTCCAGCAGAC AAACAGCATGAGAAAAGGCCGGGAGACAGTAATAATACGTGCCCATTTGCAATGAGTTACCCCAATC AAGCCCTTTTACCTCCTTAAGATGGCAGATTAGAAGACCCCTNTTCCCGAGGAGA
WI-21561	55 T G ---	---	TTTCCATTTTATCAGCCGGGCCATCAGAACTAGCATCTATACCTTCGAAACCTT/GJCTCTTAAAC CTCTCCAGGCAAGGAAAAAGTGATCATATTTGAATTTCTCAGAAATGGTGGGATCTCAAGACTT TTTAGAAAGTGCTTATTAAGTATAAGAGGCTTGAATATAATGATGATAAATGGTAGCCCTTTCTGGA AATAATTTTGTGTAATCTGTTTAAAAAGATTTTTGGATGCATTGTCCCCA

WI-21961c	200 T G ---	---	AGCTTGGCTGAAATTTGGTACTACTACCTTTGCAATTCCTTTATTTATTATTACTTTTATTTTCCGTAAGTTATGGGTACAGGAGTATTTGGTTATATAAGTCTTTAGTGGGATTTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATACTCGGTCTTTATCCCTCGCCCTG/GJC
WI-21961b	73 G A ---	---	TCCCACTTTCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATGCG AGCTTGGCTGAAATTTGGTACTACTACCTTTGCAATTCCTTTATTTATTATTACTTTTATTTTCCG/AJTAAGTTATTTGGGTACAGGAGTATTTGGTTATATAAGTCTTTAGTGGGATTTGTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATACTCGGTCTTTATCCCTCGCCCTC
WI-21956	26 T G ---	---	TCCCACTTTCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATGCG CCCACTTGGGTCTCTTCAAGTGAATTT/GJTTCCCTTCGTCTCTTAAAGCCCTTTTAAATGAACCTCCATTCCCTGTGAAACTTGCCTTAGTCTGTTCTGCTTCATGCCCTCAGTCGAATCTTTCTTTCTGAGGGCAAGGACTGAAGTGTCTGTGGACTGTAGGGTTCGACCGGTAACCTCAGGGTAACCTCCTATCTCTCCACCGGTAAACAGAGGGGTACATTATGGGGTCCAGGTT
WI-21966	148 G A ---	---	CAAAACATACATTATGGCTGCCTTTATTTAAGAAATGTTTACTGAGATCTGTACTGTAAACAACATATTTTGTAGAGCATGAGTGAGAGTGTGTGTGTGTGCGCGCGGCGACGGCATGGCACTGAGGGGATTGCAATGGG/GAJAACAGAGTAAAAAGGTATAAAACTTTGGTCCGAAATCTTTTGCTTTATTAACCTTGGCCCTGCTCCTCACAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146 G C ---	---	TATACTGGTTTTGGTTACATGGATGAATGCTAATGGTGAAGTCTGAGATTTAGTGTACCCATCACTGAGTAGTGATGATGTACCCAACTTGTAGGCTTTTATCCCTTACCTACCTCCACCCCTCCCATTTTGAGTCTG/CJCATAGTCCATTATACACTCTGTATGCCCTTTGCATACCCATAGCTTAACCTCCC
WI-21139a	165 T C ---	---	GCTCTAGTGAAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGTTCAAGTCCCTGTTCTGCCACTTACTAAGTGCATGACCTTGAGCAAGCCACTTAATTTCTGCTCCTCTCTGTGAAATGGGTACAA
WI-20317b	217 G T ---	---	TGTGGGTGACGAGTAAAGGAACATAACATTC/GJGTACAGCACTTCAGGACAAAGCCTGGGCACACAGCACTGCATGGAATACACAGGTAAACATTTTAAACAGTGGGACAAATTTAAGTACGTGGCCAGCGTGTGGTGTCTGTGGTCATTAAAGACAATGTTAAGANTCAGGAGTACTTAAGTGTAGTGGTTACA
WI-22082e	179 G A ---	---	AATTTGTCTCTTCAGTTTTTCAATTAAGTAAATCTAATAGATGATATACATATTACTGCAGATAAAACCATCATCAGAAA/GJTTTAAATTAATTCATATTTTGAGGCTACTCT CAGGACTTGGTTTGGTGTCCCAACTGCACATAAATGTCCCTTTTGTGTTAGTATTGGTTGTGTGCGTTTTCTCTTTTGCATAAGAAATATGTCCATTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGGAGG
WI-22082e	179 G A ---	---	GTACACGGGGGCTCCGCTCAGTTCGCCGCGAAGGACGTATTG/GAJCTGAACCTGGGACGAGTCTACTCTCCCCCACAGGAGCCACGATTTCAAATCCTCTTTTGCTGCAACCTCT

WI-22082b	67	C T	---			CAGGACTTGGTTGCTGCCAACTGCACATAAATGTCCCTTTTGTGGAGTTATGGTTGTGTC /TGTTCCTTTTGCATAAGAAATATGTCCATTAGTCCAGAGGCTCTTGTCTTATCCGGATGACGG AGGTACACGGGGCGCTCGCTCAGTTCCGCGCGAAGGACGTATCGCTGAAGTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAAATCCTCTTGTGCAACCTCT
WI-20993	139	A G	---			AACACAACTCCATGCTTCAAGATTCCACACCCAGATACTAAGACATATTAAATTTACAGCAAT TAAACAGTGTAGTTGGTACAATAACACATATAGCAATGATACAAATTAGGGGAAAAAACCCCTGG GCTTCT/GJTAACAAAGTGAATACATTAAGACAGATTGAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCTATTTCAGGCTTCTCTAGCTCATCCACACATCACC
WI-21723b	125	A G	---			AAGCGATTTTATAAATTGATTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTC/GJACATAAAATTAGTAGCTTCAAAGGGTTAGTCATATTCCCCAACACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82	G A	---			AAGCGATTTTATAAATTGATTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTC/GJACATAAAATTAGTAGCTTCAAAGGGTTAGTCATATTCCCCAACACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99	T G	---			CAACAGATGCTTGAGCCAAAAGCAACATAGGCAGAAATACAATTGAGAAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCCTTTACTATCCTT/GJCCCCATTTCTCTAATCTCTTTGGCCTTACAA TATATTACCTTCTAGGTATCACCTCATCCTATAGGAATGCCCTCTAGTTTAAATGTCCTGCCCCCAACA ATACTAACCCATTGAAGGATAACTATGGAAACCTTTAAATGGGACAGTGGG
WI-21006a	106	A G	---			TGACAGATCACACCACATTTGTTTGTAACTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTTTAAAGAACACATACACACATGTGCACACAC/GJAGAGGGCAAGTACAAAAATGTAACC CCACCAAGTGCATGTGAATGAAGTGCAAAAAAGGCTTCATTGCAAACTCTGAGGATCATTTCTCT CTGCTTCAGGAAAATAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138	C G	---			CTGAGGCCCTGCTCTAACTTCAATNTGACGGAGCGAGTTCTCGCTTGGAAATAACTGAAAAGATTCT TTTCTCTTTGTGTACAAAGGATTCAAATATTTTACATCTCTCTCTGCCAGTTAAACGTGCCGTGG CTC/GJCAATACACACCAAGCAAGCGTAACCTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166	G A	---			AATGAAAATGCCACCCAGAGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACAGTGTGCAGCTTTGATTCTCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACATAA CTCAGGCCACCCCTGAAATATCTGCTAGTGGG/GJAAATTTACACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACTACACATCTGCCAGGGTAATAGGCATGGGCAAT

WI-21079a	50	G A ---				AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTG/AJCGCAAAATCAAGT TGTTTTAATACCAAGTGCAGCTTTGATTCTCTCCATGAATTAAGCTGTGTGTCTCACTGTTTACA TAACCTAGGCCACCCCTGAAATATCTGCTAGTGGGAATTTACAACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI-22129a	45	T G ---				TCTGTAGATTTAGCCATGCCATATATTTAACTTTAAGGAAAAGT/GJTTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTAATAAGTTAGCTTAACAGTTAACAATTGAAGTCTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTCAAATATAAATAATTTGGTTGCAAAATCCAGNAAAGGCA TTAACCAACATGGGACTGATCTGGGGGCTTCCAACTGACTAAGGTTTTA
WI-21941	79	A G ---				TGGAGTTAAGTGGGGCTCTGCTATTTCCCCCAAGAGGACTCGGAAGATGTTGATTCAGGGCAGAGT GAGGGCAGAC/A/GGGATGAGGCTCTTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGTTGGGAGCTCACCCAGAGAGCTCACTGCATTGACCCACACCCACCACTCACC CAGCACACAGGCACACGAGGGCACACGCACACACGNTGCACTCACACGC
WI-18916b	42	C T ---				AATGGCATCCCTGTGATACCAACATCTTCAGCA/GJCTCAGCCGGCTTCCCACTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTGCCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-18916a	35	G C ---				AATGGCATCCCTGTGATACCAACATCTTCAGCA/GJCTCAGCCGGCTTCCCACTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTGCCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-19828c	200	A G ---				TTCCCTTCTCCCCAAGAGTGGCAGAAAAGCTTTGTTAACTCTCTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTGTAGCCTAGTGCAGGCTTCTGGCCCAATTTCTGGGTTCTCCCAAG CCCATGCTTCTCCACTTCTCACATCTTTACTTCTCTGACCTCACCCACCACTCACTCACTCACT JCTTTAATCTGGAAAAGAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47	C T ---				CACAAGAGTCTGTACAACCTTAGGGACACAGCCCTGCCCTGCCCT/CJTAGCTGCATGCCACCTC ATATCCACCCCATCCAGCCTCTGCCCCGACACCCCAAGGCTCCCTGCTCTGGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCTTGATCCAAACCACAGCATCT
WI-19860	51	C G ---				TTGACCTAAAGCCTAGCATAAAATAGCTAAGTAGAATGTTTCCAAAGATG/CJGTGCATCAGTAT CTCCCATCCACATAATTTCTGTTTGAATTTTGCCATTACCCCAATAAATGGTGGGATCTACCTCCCT CCTTGCAAATTTGAGCTGGNCCTCTGATCCTGTCTAAGGATCTGAAGCC
WI-19899b	80	C T ---				ACCCAGCTCCTCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAACCTGCAGGGCAAG AGGAGTAGGGG/CJTTACAGCATTTATTTCCCTCTTCACTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTCTCTTGCCACAGTCGTAACCTATTC

WI-19891c	172	C G	---				TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAAATGCTTGGTGCCCCCTCCCCCGG ACTOCTCTGTCTGGGAAACGTGGCTTGNCTCCAGACAGCTGTAGATGCGAGCTCTCTCAGCGG AGCTCCCGATCCCTCAATTTGCCATCTGTCTGACTC/GCGCTTCCCGGGCGTGGGGCGTGTGT CAGGAGCGGGCGGGAGGAAGGAAGAGATCCAGGGTCTGTCTG
WI-20155a	81	C T	---				GCACCTGTAGGGGTAGCTTCCATGTTCTCCAAAGCACGGGTGTACATTACCTTAGGCTGAOCAT TCCCTTGGGGGGG/C/TGCAAAACTGCTTTGAGGAAATNCCCAGGAGGAATAAACTAGAACGCG ACCTGCTATTTCAACCATACTATGGAGAAATACAGCTAATGAAGTGGTGGCAGAAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTGTCTGTCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91	T G	---				AGCCATACAATGCATTGCAAAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGTCAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCA/T/GJACACCAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAAGGATGCT GGGTGATCTTGTTCOCOCGACAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20270a	53	G A	---				AGCCATACAATGCATTGCAAAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCG/G/ATCAGTGTAC AATACATTCATGTCCAGGATAAGGAGCATACACAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAAGGATGCT GGGTGATCTTGTTCOCOCGACAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20622	130	T C	---				CCACITTCATATTTTACAAAATGCTCAGCGCAGCAATATGAAAAGCTTCAACACTTTCCTTTTGTA ACTTGCTGCAATAAATGCAACTTTAACAAACATACAAATTTCTCTGTATCTTAAAGTTGAAT/C/
WI-20768b	190	C T	---				TACTAATTTTATGATGTTACTCATATTTTATTCATATACTTTTAAATGACATCATTTGCCAATACATA CATTATTTCTNTAACTTTATTTTACAATAAGCCAAACATCTGTCTCATGCAG
WI-20768a	71	C T	---				TTCCACTCAAAACTCCACCCCAACCTTCTGGAAGGCGAGGCTAACAGGACCTCCTGCCTGCCTGC TCACGACTGATTACTTTTCAATCCAGCTGCAATGCAAACTGAAACTCAATCTGTATATCACCACCTA CAGGAGAGGTCTATTTCTGGGACCCAGAGAGNTCAGCACACATCTGCTGGGA/C/T/CAGGGACTC GTAATTCGCTTGGTCCAACTCTTCTATGGGGTTTAGCTGCCCTCATCC
WI-21909	153	A T	---				TTCCACTCAAAACTCCACCCCAACCTTCTGGAAGGCGAGGCTAACAGGACCTCCTGCCTGCCTGC TCA/C/T/GACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCAATCTGTATATCACCACCT CTACAGGAGAGGTCTATTTCTGGGACCCAGAGAGNTCAGCACACATCTGCTGGGACAGGGACTC GTAATTCGCTTGGTCCAACTCTTCTATGGGGTTTAGCTGCCCTCATCC
							TGTTTGTCTTGTCCAGGTACTCTACTGCTTTACATAAAATATCTCATCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTCAAAATAAGGATATTGTTGGTCACTTTTAAAGAAA TGCTCTAACATACCAAAG/AT/JAGTGGAAATCAATAGAAATAAAATATTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCACATAAATTTATATTTCTATGTATGGAAAG

WI-22202	128 A G ---	---	---	TGTTGCTTTGGTTGTTGCTTCTTGAAACATATTGGAACACTTGTTTTTCATAAGCTGTCTGACAGT GGCAATCCCATCCATCTTCAGGCCCTTTAATAAGGTCAATTATGAATCTGAATTTCTA/GJTAAAT ACTCTGGTGCAATTCATCTGCAAAAGCAACTGGCACAACCACTCTGCGGGTGACGCTCTCGG AGAACATCTAATATTGAGTCTAGTCTGTGCGGAACCTCTCCAGCTCAC
WI-22189	70 C T ---	---	---	CCAAAGGATGAAATTTCCACATTTATTTTNCCTTTATGTGAATAGAAAATGGCAGTGAAGTGTCTATG AACTGAGGCGAGGAATGGCATGGCGCTGCGGTACCAAGCCTGGACGTTGTGCTTCCAAAAGTACAC TATGTGGTGGAGACAAAGGGT
WI-22283	109 T C ---	---	---	GGGAGGCATCATAGAAAAAAACCCTCAGCCAGAAAGTTAGGACATTTGATTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCGCAGGCTCTGGTTGTC/JTTCAATTTGCAAAATAAAACCCA GACCGGTCACTCTTCAGTTCCCTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACCTCAACTCCAATGATGCAAAAAG
WI-22290a	136 C T ---	---	---	GACGTCACTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTTATGGCCTCTAAGCACCG GCCAGTAGTGGGAATGCCACATGCAATGGTGAAGTGGGATCTGGGGGGTCAAGGAGCTGACGCTTGTCTTT [C/T]TCCAATCTCTCTCTTAGCCAGAACTTTGCGAGAGCCCTTTNATTTCTCTTCCCTCTATTCC CCTCTTTCCCAATGTCTAAGGTCCCAATTCAGACCCCTCCAG
WI-22292	53 A G ---	---	---	CCAGTGAAGGGTTACAGCCATAGTGAGGTTCCCCCATTTGCTCAGTACCAGA/JGJTGTGAGTAC GGTCGTTAAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186 C T ---	---	---	ACCTTGACACCTGCCATCCGGTGCCATCTCTCGGTGGCACATCTATACCCACTCTGGCTCTGAAAG GCTTGTCAACCAAAATGGCAGCTGGGGTAAAGCATATTTAAACAAAGGCTCCAAAGGACCCCTT TCACTTGGGTCTAGCATCCAGCTCTCTCAGCAAGGAGGATTGGTTC/JTCTTGTGTTTTCTG AACAGGCCAGGGCAGCAAGGCATGCCATCACTGCAGCACTCAACCT
WI-22395b	127 A G ---	---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTTCTTCTTGAATATTT GTAGGATGGATGAATTGAAAGTGAATTAAGTCAAGTAAAGGGGCAACTCTTTAAT/JGJAAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	---	TTTATGCTCTGAGTGCCCTCACCCAGCTACACTTTACCTTGTATCTATAAAAGTGAATTTAGAGT AAATACATTGGCTGTAAAGTCG/JGATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGTGCAAGTTTCTCAGTG
WI-22419b	67 T C ---	---	---	CCCTCTGGACAGTTTGTCTTATGTGTTTCAGACAATCAAGNTGCGCTTCCAGGCACAGCCAGTGCT /CJCTGGATGGCATCAGCAGGCTCCCTGCCCCGCCCTTGAAGCATGGCTGTGTGACAGAT
WI-21342d	59 T C ---	---	---	ATTTTCCCTTCTGTGTTTCGTATTTCCCTTTTGTGAGTAAATNAGCAATACACTGA/TCTJGGAA ATCTGCATGATTAATAACATTAAACAGTTTCATAAACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCAAAATTAGGTATCCCTCAAAATGGCACATTTCTCCTCCTAGTT T



WI-21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACACATTGATCTTAGTTAACAGTCTTGTAGTTCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATTAGJICAGACATTGCCTGTGCTTCTTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-21763a	135 T C ---	---	CATACCCCTTTAGGTGCCACACATTGATCTTAGTTAACAGTCTTGTAGTTCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT T/CJGCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---	---	CAGTCCATTTGAGTCCCAGTCGAGGGTGCATTCTTCCCTTATCTTGTTCCTTAAAGCCACTTGGGTAA/C/] TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTCAAGTCCCTGGAGGGAGGCTTCTGCG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGAATACAGTAC TTCCTTT/CJGAAAAAATACACAATGGGAAC TGACA
WI-21965a	112 A G ---	---	CAGGTCCACCCAGAGGCTTTTATTCAGCCACTCAGAACCTGGCTTCTGCTCCAGGCACTGAACA CAGTCAGGCTCTTAAACACTGGCAGGACCTCCCCACAGCQJGJCCCCACAGGGTCTCTGTT TCCCAGTCTGATGGATTACAGCAAGACCTTACACATTCACCCACTACTCTGCTGGAGAGGGGTC ATAGGCAGCCTGTGGTGCCAGCTCAGTGTGACACACTGCCAATGTCG
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCTTAGTCAGAAAGTCTATGGACTTCTTCTTAAG/C/GJTGTTCTATGATCAGAC CACCTCCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAAGGAGCCTGAGAAGAAATTCACAACCTATTGACTATACAGAG TCTTCAATTCCAAACACAGTTAATAGTAACCTGGTGGCACATACACATGCATTGAATACTCTGTAT TATTCAGTAACTAAAT/CJAGGNTCCTGCATCTCTTTCACA
WI-22250b	132 C T ---	---	ACTTGCTTTCAGGCAGGCAATTTCTGGGATCTAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCAGTGTAGTGGGTATTATGGGCTCTGCTCCTCCTGGCTGTGTATG/C/T/] GGANCCAGGAGTGGAGAGAGCCGTGGAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGCTTTCAGGCAGGCAATTTCTGGGATCTAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCAGTGTAGTGGGTATTATGGGCTCTGCTCCTCCTGGCTGTGTATGCG GGANCCAGGAGTGGAGGAGAGCCGTGGAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCCATCCTCCTCTCCAACACTCCAGGCCACCCCTGGGGCCAGAGCAOCTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCAGGTTCTGGCTCTCAGGACGTCGCCAGCAAGTGGA GCCAGAGGTTTCTGGGACTCCAGCCAGGGGATGAGGCCAGCCCCAGAACCTG/CJ/AGTGGCTTC TTTGACGGGGCCCGCTGCTCAGTCTGCTGCTGCTGGAGGTGAGGAAGGAGGT

UTR-04932-2a	149	C T ---	GCAGCCATCCTCTCTCCAAACCTCTCCAGGCCACCTCTGGGGCCAGAGCACTCATGCCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCCCAGGTTCTGGCTCTCAGGACGTGCCAGCAAGTGGA GCCACAGGTTTG[C]/TTGGGACTCCAGCCAGGGGATGAGGCCACGCCCCAGAACCTTGGAGTGCTTC TTTGACGGGGCCGCGTGCTCAGCTGCTCTGGAGGTGAGGAAGGAGGT
stFIBBb	412	G C ---	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCCTGAGCAGCTGTGATTGTGCCA CGGAGGATGAGCCCTTTTCCACGGCCCTTGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACCCAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCAGTCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stFIBBa	341	T C ---	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACGGCCCTTGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACCCAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stGLV2	61	T C ---	GTCAAGAGGCGCCTCTCGGGACGTCTCCACATGGCTGGCTCTGCTGCTCTCACTC/TCTCTC CTCACTCAGGACACAGGTGACGCCCTCCAGGGAAGGGTCTTTGGGACCTCTGGGCTGATCCTTGGTC TCTGCTCTCAGGCTCACCGGGGCCAGCACTGACTCACTGGCATGT
stSG1001 7c	70	T C ---	GTTCAGGCTCATCTTGAACCTCTGGTGTCAAGCGATCTCCACCTCGACCTCCAGGGTGTGGGAT TA/T[C]/JAGGCATGAGCCCCACACCTGGACACAAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAACATAAAGTATGATGGCTTACTTTCTAATCC
stSG1001 7a	33	G A ---	GTTCAGGCTCATCTTGAACCTCTGGTGTCAAGC[G]/AJATCCTCCACCTCGACCTCCAGGGTGTGG GATTATAGGCATGAGCCCCACACCTGGACACAAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAACATAAAGTATGATGGCTTACTTTCTAATCC
stSG1002 3	63	A T ---	TAATGATAATTAGGCATTCTTCCACACGAAGATGACACAATTGACCCCAATATCATTTGAGGC[AT] AACAGTTTGGGCTGTTTTCCAGTAGTATGACAGTGA
stSG1009 6	36	G C ---	GTGGAGAAAGATGCTTTCTCCTCCCTCCCATGAC[C]/CJGGCTTCCGGGGCACCCTGTGCGTTTTC ACCCGAGACGGCCTTTGTAGGGACCCACTGCCCCACTCCGCTGCTGTGCGTGGGTTCCGCTCCTAG GGCTCGAGTGTTAAG
stSG1011 8	107	C A ---	TAGGCTTAAACCTGGAATCTACAAGCCAAAAGTCCCTCCCTGCCTGAGGGCAGTAGCCCTCCATTGGGC ACAGTCCAGACCCAAAGTCAAAGATGCCCAATTCTTGG[C]/AJCTCAGCCCTCAGTCTCTTCAATTCC ACCAGGCCGTGCTTGTGAGTTTTTCTCCAGTGAG
stSG1012 0	89	T C ---	TAGTAGTAAGAAAAGCAAAGGAGGATTGCTTATGCGATGACTGTTTACAGTGGTGTGAGACTATGC CGTGTTCACGAACACTTTAATAT[C]/GTTGTGTATCTGATTTTATCCTCGTCTTACAAAATG
stSG1017 8	42	C T ---	TTGAAGCAATATTGCTAGCACTCTGCTGGACATTAAGTCCG[C]/TGGGAGGAGAAAGTGAACAGGAA TCGATTCTTTGCTTTTAAGTCCCTTAGTAGGAGATGTTAAATACTTGGC

stSG1019 3	136 GA ---	---	---	GGAAACAATACTACCTAAGGACAAAATACTATTATTAACAAAAAGCTCTTAGTGATATTTGTGTAACACATTTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAAACTTTTAC
stSG1020 2c	143 GT ---	---	---	TTG/A]TTTGAAAACTGAGATTAAAGTTGCAAACT AAGCTAAGTGGTGAATGGTGCCACTCAAAGGCTCTCCGAGGGAAGCTCAGTCCCTGGCTTGGGAGAGTCAGCCTTGGTCACCTCATACGGGGCTCAAGCTAAGGGCTCAAGGGAAGCAGTCCCACTGCTTCTCGCTGTCA/GT]CAAGACCAACAAGGCAGATGCCACTGCTGCTCTTTCCCTTGTCTACTTTCT
stSG1020 9b	75 AG ---	---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTCATAATAAACTAATTCCTTAAGATCCACATTTATTTTTA/G]CTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1020 9a	34 CT ---	---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTC/TAATAAACTAATTCCTCTTAAGATCCCACTTTATTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29 TC ---	---	---	TACTAGACATGCAAAATGAGAAGATTACA/T]C]GTGAATATTTAAAGAAGTTATATTGTTTGACATAAATATGATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTTCTGA
stSG1025 2	108 AC ---	---	---	ATAGGTTTCAGGAACAAAATCATTAATGGAATAATGAGAAGAAATTCCTTTATTTTGGACCAATTTTAGGCACTTAAGAGTTTCTTTTCTCTCTCCCTTGATCA/A]C]AGTGAAGATATGATAGGGAATTCAGAAATTTCTCTCTTG
EST10915 0	123 AC ---	---	---	CTGTATTAAATTAAGAAGGCACATAATTAAGGGACGGGAAAAATCTACCTGTACACAAAAATCTGTACTTTAACAGCATCTTCAATAAACCTTTAAAGGATAATGGTTACGATCATTTTAAAG/A]C]ATTTTAA
EST11023 1	166 TA ---	---	---	GAACTGAGTTATTTGGAC TTTTTTGTTAAACCAACCCTGAAAGTTTCCACATGTGAATATAGATACACAGTGAACAAAAATATGTGGCCTCCCATGTACATTTGGTTACCTATGTACAAGTATCTATACACCAAGTAAACAGCAGGGCAATTAGTCAATTAACAAAAATAGTACATGTTA/T]A]GTGTAATAAAAAATTAATTTACAAAGGCTTTTCCACTCGTGGATTGATTCCTTTTGGAGGAGGGAGTAATCCTGG
EST14096 8	71 GC ---	---	---	GGGATGTATATTACAGATAACACAACTCACAATATACCATCAGACATTGAAAACTAAGGCCATTCTGTGA/G]C]TTATTTTAAACTTGGTGTTTGCACATAATGATCTTAAAAAATAATGAATTACCAAAACCAAGATTCTCTCTAAATGAAAAATTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATCTGAAG
EST22113 6c	125 CA ---	---	---	TGCAAAATGTGAGAAGGCAGCAGGGGCCAACCCCTGGACCTCATCTCTGTAGATGTGAGGTGTCAGGGATGCTTAAGTCTTCTCTGGCAGAGACCCGAGGTGCAGAGATGATTTCTTCTCA/C]A]CCCTTCTCAGGGTCTGGAG
EST22555 7	60 GA ---	---	---	TCAAGCATGTGTAAGGCACCTGCCCCGCCAGACCCCTTCTAATCTTGCACACTGGAAGGTG/A]AAACCTGGGAGAGAGAAGACACTCCCCCTCCCTAGCTTCACTGGGCAACCCTCCAAAGATGAGCATTCATCTTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGCTCAGAG

EST22917 6	74 C T ---	---	---	GTAAACCTTGCAAACGCCATGCTAAATGAAGCCTGACTGACCAGGGGCTCTGGGCTCTCAATGCA ATAGAAAC/TTGACATGGGGCCAAAGACTTCCAGACAAAGCAGCGAAGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGAACCTTAACCCCTCAGGCTGCTCTACTCA/AV GTTGGTTTGTAGCCTCACTGCACACAGGAAGCTTTGGAATTTGGAGGCTCCAAGTCACTCTCCA
EST36745 3	56 A G ---	---	---	GAGGGGAACCTTCAAAGAGGATCCCAACAGTGAAGCAGAAATCATGGGGCAAAAGTCA/GJCTATGG GGCCAGACTGAGGTGGACCAACACAGCACTCCAAGCTGGGCAATCCCAACCGCTGGTGAAGCGGC ACAGCAGGAGTAGOCAT
STS- R37410c	201 A T ---	---	---	TGTGACCATAACCAACCTATGCAATAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCAATTTTTCAGGTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAAATACAAATGTGTGATCTCCTGAGACACATTTATAACACATTTCTGGTATG T/ATTTATGTGAGTGGTGTCTAGTGGCCAAT
STS- R37410b	139 G T ---	---	---	TGTGACCATAACCAACCTATGCAATAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCAATTTTTCAGGTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATG/TTGTTTGAATAAAATACAAATGTGTGATCTCCTGAGACACATTTATAACACATTTCTGGT ATGTATATTGTGAGTGGTGTCTAGTGGCCAAT
STS- R37410a	48 C T ---	---	---	TGTGACCATAACCAACCTATGCAATAAAGAAAAAATCCTCA/CTTAAAAAACAACAA AAAAACCTTTGCAATGCTATCAATTTTTCAGGTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTT GGAAATTTATGTTTGAATAAAATACAAATGTGTGATCTCCTGAGACACATTTATAACACATTTCTGGT ATGTATATTGTGAGTGGTGTCTAGTGGCCAAT
STS- R42778	74 C T ---	---	---	TATCGTGGGAAGTTCCAACCTCATCTATGCTGCTTTCTACTTGCTAATATTGGATGCTCTTGCCA GGCTC/CTTTAAATTTGTCTGTAACTGGGAAGAAACCTTCTACTCTCCACAACCCCTGAA
UTR- 04350	125 C G ---	---	---	CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGGATGGTGAAATGTTCCGACCTAGATA/C/GT/GACGA AGGTAGCAGCACACTGTGAGTGCACATA
stSG1026 6	55 T C ---	---	---	GAAATAAACTAAACTGCAAGCAATCACTGTTAATAAGAAATTTCTCTGTTT/C/GACAGTTG AAGTGGGTGTGAGATGGGATAGCAATGAACAGTGGGAGCCAATGAGGTCTCAGAAATGCGGGCAAA CTCCTCTGTGAAATGTAT
stSG1028 2	70 T G ---	---	---	GTATAATTCAGCATAAGCCAAAGCCTTTTAAAAATAACCAATACTATCATTTTATGAAATCTTTACA AGAT/GJAGCAGACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1031 0	128 C A ---	---	---	CACCTTAGATATGAGAAATGGTTTAAATGGACACAAAGGAGTCAGCCACGTTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTATGATGCAATACAGCAATAATTTTTTCACTC/A/JTG TCAATGCCAATGCATTTGAAAGGCCAGAAAATGAGAAAAGGATAACAACACTTTTGATAAAAAAGGTA AGAATTTCTGTGTG

[illegible]

stSG1847 b	95 G A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAATTT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTGCGTTTATAGACATTTGAA TCATATCTGAATGACTGACTGTTTCCAAATGTGAAACCAAAATTAATAAATACTTGATCACTGTGCT TCAACACAACTG
stSG1847 a	49 C A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAATGCTACC[C/A]CTAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCAGTTGCGTTTATAGACATTTGA ATCATATCTGAATGACTGACTGTTTCCAAATGTGAAACCAAAATTAATAAATACTTGATCACTGTGC TTCAACACAACTG
stSG1897 a	83 A G ---	---	CTTAATGCCCTTCTCTCTCTGCACAGGAGACACAGATGGGTAAACATAGAGGCATGGGAAGTGG AGGAGACACAGGACT[A/G]GCCACCACTTCTCTCCCGGTCGCCAAGATGACT
stSG2022 a	86 T C ---	---	TGCTTGAGGTTTCAAATCTGAGATATCTATGGCAAGTTTATAAAAGTACATTGATCAAGGTACAA TTTTAACATTAAATATACAT[C/A]TTCCATAATCTCATCTATTAACATTAAACACAGGCCCTTTGTTGT TGTTATTTTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGGCCCTCAGTTGGGGGTTGAC T
stSG2076	104 C G ---	---	AAACGTTGTCCCAAAATTGTGTTTCAGTTTCACAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAACACACTTAAGAATATATTTGACATT[C/G]ACATCACAGTGGGCAATTTT
stSG2108 c	71 A G ---	---	TTGAGCAACAATGATTGCGGAATTGGCAGCTCCAAACCAAAATGATT[C/G]AGGGGCTCCACAG GAGC[A/G]TAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTTATTTGGTCTATCTTATTTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 T C ---	---	TTGAGCAACAATGATTGCGGAATTGGCAGCTCCAAACCAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTTATTTGGTCTATCTTATTTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 A G ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAATAATCTCAGAATGGCAGCACCACTGGCATGGCGATGGTGCAGGTGGT GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[A/G]AAGTTCCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCATCTTGTTGCTCTG
stSG2141 a	113 C/T ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAATAATCTCAGAATGGCAGCACCACTGG[C/T]ATGGCGATGGTGCAGGTG GGTGCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGTCCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCATCTTGTTGCTCTG

stSG2148	50 A G ---	---	---	TGGAAACAACCGGCTATAGTCTGAGTCATATTTTAGACCGTGATTTTC[A/G]AAAGAAACAATAA ATGTGGATTAGAAAGGAACATCCATTACTGTATTTTCGATACTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68 C T ---	---	---	CTCAATGAGGACTCCATCAGCCCAAGCGTTTATATGGCAGATGAGCTGTACAAATCTGTTGTGTGCT [C/T]GCCGCGTGACTAGCTAATGCTACCGGGTTGGAGCGCACACGAGCCAGCCACCTTTTCCAT ACCTGGCAGAGGGAAGGGAGTGAAGGACCA
stSG2189	41 C T ---	---	---	CAAGTGGTGAAGCTGGATTTGAGCCTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAACATCATCGCTAACTTGAGCACCTTAGTGTTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTGCGAAC
stSG2200	49 T C ---	---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGGCTGGTCTGTATGATG[C/T]TTATATTTATGTAT AATGCTTTACTGATGATACCCCAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	---	CATTTTCTGCCTCTGCTTCCCAGTACTACCCCGTCCAGCACTGCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAG[G/T]AGAGCATCTCTCAGCCCTGGGAAGACAGTGTGGGAGCTTCAGCT
stSG2257	65 A C ---	---	---	TCAGTGATTGTAGGAGCTGGCTAAGTCATGCTAAACTCTGTGAGGCAGGCTATCAGAAGGGCAG[A/ C]CTGTGAGGAACTCTCGCCAAAGCACTGGGCTGCTCTCAGGCAGAAATTTCTTCCT
stSG2306	67 A G ---	---	---	GTCAATCAGCGTAGAGGTCACTGGTATAACAACAGTAGCTATATGATATTTGGGAACTATTTTACA [A/G]TATGCTCCCATTTGGGTTTTCCAAACTGATACAACTGAGGTGAACACTTTCACCTGTTTCACAG TTCTCTCCAGAGA
stSG2334	70 T G ---	---	---	GAAAACTACCCACAGCATCATGTTAAAGAGAGAGATGAAGAAAAAATCCCCGCAAAAAACA AAAAAT[G/T]GCAGTGGAGGGGCTGTGGGAGGGTGAATG
stSG2339	63 T C ---	---	---	AGAGCAGAATGGTGAATCAACAAGACCTCAAATTTGCTTGACTGCAGAAGTAAGTGTGCTAC[T/C] GTTCTCAGAGTCACCATACGGTGACTGTGCTATCTGGCTGTGCTTCTATTCATCA
stSG2465	76 C T ---	---	---	CAAGACTAAGAGCCGCAACCCGAGTGGTCCCACTCAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTTCAAAGTGTGGGTATGCA
stSG2549	140 T C ---	---	---	TTGCAGGCTTGTTATCCACAATAACAAGTCATGTATAGAGAATGTGAATGATACTTGAAAAACCAA GATATATAAAATATTGAAGTCATTTATGCCCTTTTGATGACTGGTTAAATATGCAAGCAGCTAAAG GAATAT[T/C]TACACCACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	---	AATTGCCAATGGAAAATTCACAGAGGATTTTAGACCAACTTTGCCCTGTTGCATTTCCAGTTTGGT CCCAATATAGGCCCTCTGCAAGAAGAGATCAATGCCGAACCCGAAGTGTGAAGCA[T/G]GAACAATC CCGGCCCAGATTAAATTATT
b				

stSG2577 a	121 C T ---				AATTGCCAAATGAAAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTGCAATCCCGTTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGC/TATGAACAATC CCGGCCAGATTAATTAAT
stSG2700	58 G A ---				ATCTCTGACTGCTTTAGTGGGAAAGGAATCAATTAATTAAGAACTGTCGGCCCCG/GAAGTCAC TCAGCGTTGCGGAAATAAACCACCTGGTCCAGAGAGAGAAAGGCTACTTTGAGCCGGACACCA
stSG2724 b	101 T G ---				AAACAAGCTTTGTCATTTCCACTACATTTTGTGTGCTTTTATTAATAATTTGCAAAATGCTATAAT TTAATACTTAATCCAAATGCTTGCAATAATCAT/GTTTTTTTAAATCCTGGGGTGTGAAAGAAC
stSG2776 a	65 G A ---				GTGGCCGATCTTTACTTTTCCAGAAAGGCGGTAATAAAACCTGTAGAAAGTCTCGAATATGC/G AJATTGGCCCTTTTGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAAACCAAAAA ATATCCACTAATCCCGAATATAGTAACCCGTGCTTGTCGGAATG
stSG2791 b	109 G T ---				AAGGAAAGGTGGAGGGAAGGAAGAAATTAACAATGGTTAGAAAAGAGCAACTAAAGATTATTT TATTACTTCTGAACGGTAAACTAGCAATTTTAATAATTTG/TGGGTCCACTTAAATCTATTA AAGCAGAAAGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791 a	100 A G ---				AAGGAAAGGTGGAGGGAAGGAAGAAATTAACAATGGTTAGAAAAGAGCAACTAAAGATTATTT TATTACTTCTGAACGGTAAACTAGCAATTTTA/GTAAATATTGGGTCCACTTAAATCTATTA AAGCAGAAAGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2826	85 C T ---				CCGCAATTTCAACACACATCTATGAAAACCTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAAACAA/C/TJGAACAAAAATAAAGAAAGAAAAACCCATGAAATGCCCCAGGTTTA ATTTTTTTCC
stSG2850	88 G A ---				ATGGGTGCATTGTAAAGGCAATTAATACTTTTTCAGGCAGGGCTGGCAATTTAATGAGCTGA TGTGTCCCAAGGAGACGGCC/GA/GGCTCACACATCCCATCAATATCTCTCCAT
stSG3031	71 T C ---				ATACTACGGGGCTGAAGGCAATGTGAAGAGTGAAGTCAAGTCCCTGGCATTTTCTGTGGTGTGAGC AAAT/C/GCCCCCTTTATTTAAATGATTCAGACATCTGGGCAGCATAGCT
stSG3058	81 G A ---				GTCCCAACTCTCTCTCTCTTAGAGAAAAAACTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAAGTCAAAAC/GA/TGAAGAGCATCAAAAGCCAAAAAGGCAAACTGGCTGAGGC
stSG3092	94 T G ---				CAGCATCTCCAGAACATTCCTAGAACTGAACCATCTTGTCACTATTGAAAAACAAAGCCAAAGTTC CAAATCCAAATAATAATGAACGTGC/T/GJGATAAACATCTTCTTATGTTCCAGCCCCCTACTTT AGTT
stSG3230	95 A G ---				AAGAAGTACTTTGGTAGCTATTTAATAAGAGGGGGTGGGAATGAATGTGAGATACGAGCACCTG CATCTTTTAGTCAATTGTCAGTGGAGTCA/GJGTGGGGTGTAAAGTGTCTGAACGTGAAGTAG
stSG3245	160 G C ---				ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTAGAGCAAGAGCCCTGCTCCAGGGGCC CAGGTATGTAGAGGCCAGTGGGGTGGCCACTTGGTGTCTTACCAACCCCTGCCATCCAGTCTG GCCCCAGTACCTACCTGGGAGGTG/CJ/TGTAAGTACTTGGCTTAAAGTACTTATGCTTTAT



siSG3265	42	T C ---			AGGTGAATGAGTTACTAAATGTAGCATTTATTTATAAGGAATG/C/GCAATGTGTAATAGTTTCTCAG TTTTCAATATGGAAGATGATGATTTAGCCCAATTCAGTGTATGTTCTTAAATAACACATCGAC AGGACTGCTGTTGAGTACATGAGGACAGCTTTTTCAGGGCAATGGATTTCTTGATAATGCTAA ATCTGCTTGTGAGCTGAATTTCTGGGCTTTAIGGGCAGTGTGGTAAAA
siSG3269 b	141	C T ---			TGTAATGAGTGTGATCTCTATCCATCCCTCCCTGAGCCTGAGCTGCTCTCCAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAGTTACCCCTTAAGCTTGATAATAGCTCCATAGCCATGCTAAA GCATGA/C/TJTGATAGATCCCAAGTCCCTGACACATTTTCTCTAAGAAACT
siSG3269 a	24	A G ---			TGTAATGAGTGTGATCTCTATCCATCCCTCCCTGAGCCTGAGCTGCTCTCCAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAGTTACCCCTTAAGCTTGATAATAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTCTAAGAAACT
siSG3284	130	C T ---			TTAACTCAAGAACTTTCAGTTACAGGAAGATTATCTAATATTAATGACTAAATTACAAAAAGC ATAAATGTTTGAAGCCATTTTAAAGTTGTTTTGAAATCCATATTAGCACTCAGACTTCCCCA/C/TJ TCCCTAACTTTTGTAAATGCTGTATGGGACATTTGTTTGTATCTACCC
siSG3292	99	A T ---			GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAAAATCGGTACATGAGGCTTAGACATA CACATCAATGGACAAGTGACTTAAATATCTAA/JATJACAAATCAAAATAGCATTTTCCTAACATCAA TAAATGTCATATCTTTAGCTCTCACT/C/CCAGTGTATCCATTTTCCCAAGCCGTAGAGCTTTTCTG TTCTGTAGATTTGCCCTGCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTGAGCTTCTCTC ACCTAGCATGATGTTTTCAAGACACATCCATGCTGTAGCATGCTCAGTGTCTTCTTCTTTTAA GATCCCCAGTATTATTTCTAAATGAACTTTGTTGTGGAATAAAAATCTGAGGACCCTCAGAG GG/C/TJATAAGGGAACCCCTTTTGTCTTAGTTTCAATAGGACTTTCT
siSG3369	69	C T ---			CAAGACTGTAAAGAACGTAGGCCCTTTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCCAGGACTCAGG CTTCAGCTTCACAAATCCCGAGGAAAGGAATGACATTTCCAAACTGTCACCTTTGTAGC/G/TJCTGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
siSG3398	125	G T ---			TCCTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCAGG/J/GJCTCACTGTAGCCTGGACCTCC TGGGTTCAAGTATCCTTCCACCTCAGCCAACTGAGTAGTGGCCTGCAGGACAAGTCACCATGCTTA CCTAAGTTTTGTAGAGACAG
siSG3416 a	43	A G ---			GTAAGACAAGGTTTTGCTATGTTGACCAGGCTGCTTGAACCTCTGGCTTCAAGCGACCGTAGCCA CCTTGGCCCTCCCAAGTTGCTGATATTACAGGTGTGAGCCACTGCCCGCCGACTTTTAACTGAAT GTTGAAATCAATCTGCTCTTTGCTGGGTAAACACTGAT/J/CAAGTTGCTTAACTTTGTGAAACAC TTTCTTATCTGTAAACAAATGGACAACAGAACATTTTCTTCTCTC
siSG3424	173	T A ---			GTTTCATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTGAGGTGATGGAGGCGCTCAGAGA ATGAGTGGCAGAGAGGGGCCCT/J/AGAAATAGCTTACTCTGTTTCTCTAIC
siSG3436	88	T A ---			

stSG3463	103 C T ---	---	GATACAGAAGATAGTGTGGTATGGATGGATAGTATGAAGGACAAATAATACAAATATATTTATTG AAATAAACAAAAATGCATACACAGCTCAATGGGTCACTC/TJGGAAACAAACTTGTCTGACTATATTA CTGA
stSG3491 b	71 G A ---	---	CAAGATACCTTCATTGTCTCTAAGTAGTGCAGTGTGGCAATATTTCTCAGCAACAGGACGATTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAACTCTCTAATCTTTTACTGGCACCTGTGGATTCTATTAACTCATTTATACTATTTTCTGTGATG ACAGAAAAATAAGTTAAC
stSG3523	33 C T ---	---	TAGCCATCTTACTCTAGTCTTTTTGGGTTTTA[C/T]GCATATATGTGTACAAACACACACACACACC CCTAATTCCTCAAAATGCTCTTGGCATAAGTTTTATCTCTTACTGGTCTC
stSG3536	213 A G ---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACAGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAACCAAAATACAGAATGGCTTC TGTGATACTGGCCTTGTGAAACGCATCTCAGTGTCTATTGTTTATATTGTTAAATGAGCTTG TGCACCATTAGIA/GTCTGCTGGGTCTCTCAGTCTGCCATGAAGTATG
stSG3583	112 G A ---	---	GAAAAAGCTTAACATACGATCCATGTGCAAAACCCAAACACAGGATCTACGAACCTCTGGCATGCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586 a	60 G C ---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGTGGTGG[G/C]ACGG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAAA
stSG3589	101 T C ---	---	ATATAGTGTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAGGCCAAAAAAGT GTATATACCAACCCCTGGCACAAAAAACCCCAATGA[T/C]CCTATTTCCAAAGAATGTATCCAGATGAAA GTATCCAAACAACAAAAGCTATATACAC
stSG3590 a	70 A T ---	---	GAGAGATGAGCTATTTATCTTTTACTTAATGAAGATGAAGAAATGATCTTCTGTCTTCTAAAAA AAA[A/T]TTTCTCTGATGTCTCTTGACCCTGTAGGAAACACATTCAGTTTCTACACT
stSG3619	78 A C ---	---	CAGTGAGACTTCTCATTTTATAGCAAATACATTTTTCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCAATTTA/CJAACAAACTTCAGAGAAAACTGGGCTCTATATATTTAAG
stSG3644	40 T C ---	---	ACATATGTAAGTGCCTTAGTAGCCATATTTAGGATGAGAT/CJGGATTGAGAGGCATGAACCAAGG ATGCGTAATAATCATTTATGAATAATAAGTTATCTGGGGAACGGCCATTTGTCCAAACATTTACTAA GTGCGCTACTA
stSG3646 c	70 G A ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAATATGCTTACT GGT[G/A]ATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55 A G ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATA[A/G]TATGTCCTT ACTGGTGATATTAACTTTGATACCTGGTTAAGATGGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43 A T ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG[A/T]TGATAACAATAATATGTCCTT ACTGGTGATATTAACTTTGATACCTGGTTAAGATGGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85 A C ---	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCGGATGACCATCCAAACCTGGACTCACCT GAAATATCTACGAGGC[A/C]TCGCCCTCCGAGACTGACGATTATTAAACACCCACACGGAAAAAGG
stSG3693 a	30 C T ---	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCC[C/T]TCTGAAAGCCGATGACCATCCAAACCTGGACTCA CCTGAAATATCCTACGAGGCATGCCCTCCGAGACTGACGATTATTAAACACCCACACGGAAAAAGG
stSG3698 b	145 G A ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCGAGGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCGAGGGTTG[C/G]TCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGATACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107 C T ---	---	ACCAGCTCATGTGCAGAGGGTCTCCTGCTGGATCCCCAACTGGAGGCATCCCTGGGCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104 G A ---	---	GCCAAACAAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTAA ATCAATATATTATTACAGCCAACAGCAACAGACGCC[C/G]A/JACAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGCACATTTA
stSG3751	128 G A ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGGATATGGTCCC[G/A]TT GCTGACTCCATGTGTGCAAGAG
stSG3787	49 T A ---	---	TTCTGTGCAAAAGAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTA[T/A]AAGTTCCCTAAGA CACTGAGGGCATAAAACCAACAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCT
stSG3880 b	115 G C ---	---	GACAAGAGGGAAGAGATCGCCACAGAGACCGGGCTGGGGCAGCTGGGGTCCCTGAGTGCACGGCGC CACCACAGTCTGTGGTCAAGGCCCTCTCTGGGAGCAGGTCTA[G/C]GGCACGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCCCT

stSG3880 a	36	G C	---	---	GAC AAGAGGGAAGAGATCGCCAGAGACAGGGCTG[G]CGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACACACAGTCTCTGGGTCAAGGCCCTCTCTGGGAGCAGGTCTAGGCACGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGGCCT
stSG3895	44	A G	---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGT[G]GJTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATCAATTAGTGTATCACCATTGGGAACAAGATGCTGATTCGTCACCTG AAAAT
stSG3902	104	T C	---	---	TCGTGTGAGACTGGAGAGACCAAGGTACCAAGCACCGACTCTGGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTCACTAAATGTGAACCTGCTTTCTTTTC[C]TCAGCTCAATAGCTTAACATCTAAATTC ATGTTGCTCCCTTTGCTGGACAAT
stSG3935	50	G A	---	---	GGGTGCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC[G]A]CTAGTGTGCAGGC TCCTCCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCACAACCTTCCCTGGACGT
stSG40	25	A G	---	---	GAGGAAGAGGTTGAAGAAGTGTGA[G]GJAAATATATTTAAGATTTCTTGGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTAGAATAAGGAACAAAATAAACCCTTGTGTATGTATCA CCCAA
stSG4009	32	A G	---	---	GTGTGGGCTGTCTGATGATGAATGGCGCTC[G]GJ]TACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGGCTTTAAGGGCTGAACCATATCTGAAGTTTCCCACACTGCTTACA
stSG4033	123	T C	---	---	AGAAGCCTTGGGGACAATGGCAGTGCCTTTCTGAGTAAGACATGAATGCCATCTCGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAACCTAATGTTTCAAGCATAAAGGTACTTTT[C]JGTGAAC AGGTGGGCAACAC
stSG4038 a	29	G A	---	---	GCTGAGAGCAGGTGTACAGCCACGCCTG[G]A]CGCAGGCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCAGGCTCCCGGAGAGCACTGAGGGTTCATCACT
stSG406	53	T C	---	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAGCTAAACGAACAAA]T[C]JGGTTTAGTT TTGCTGAAGACTGGCTTATTAAATGGACAGCTTTCCTAACAGAGATTATTAACTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55	G T	---	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGCTAGATGATTAG[G]TATAAAAA GTTTGCTTCTGTAATACITTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4095 a	27	A C	---	---	ATCTGGGCTGAATTAGTCAAGCAGGTC]A]C]GATACTATTGTCTGCTAGATGATTAGGATAAAAA GTTTGCTTCTGTAATACITTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4120	65	G A	---	---	TGCATGTTCCACATCTTTCATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC[G] A]CTTTTCCCTCAGAGAGCCCCACAGITTAACACGTTCCAGCACACCATTAATCCACCGAGCT

stSG4128	54 A G ---	---	---	CTTGGCAGATAAGGGACTCGTTTCAGAGATATGACTTTCCTTTGTGTACATTCTT/GTATATTATTT TACTTCTCTGAAATGCCACATAATTTGCAATAAATGATTCACCTCTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAAATGTTCCAGAGGG
stSG4209 b	128 G A ---	---	---	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAGC AGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCCTTCAGAGGCCGACTCCCTC[G/A]GC AGGGGACACACGGAGGACAGGTCTTTGATGCTCCGAGAGCTGAGCTCCATTCCA
stSG4209 a	65 G A ---	---	---	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAG /A]CAGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCCTTCAGAGGCCGACTCCCTCGGC AGGGGACACACGGAGGACAGGTCTTTGATGCTCCGAGAGCTGAGCTCCATTCCA
stSG4254 b	31 G A ---	---	---	CATTACCCAGAACGCCATGGAGGACCAGAGC[G/A]CCACGGCCGGGACTCCCGCGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCGGGGGCTCCTCTCCCGAGGGGCGAGACGTGAC TGGGGGACCATGGCCGAGAGAGGATGACCGGTCAIG
stSG4301	81 T G ---	---	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGAGTGTGGCTCCACACTTTCCAT TTAAGCAATAAAATTT/G]AGCTTCTGAGTAGTTGTTCCAGTTTACCCTCAACATTTTG
stSG4331 b	71 T G ---	---	---	CTCACAAGGGCCCAACACAGAAAAAGATACAAATACATTTCAGCTTAATTTAGTTTATGACAC AGAGT/G]TTTCAACAAGTTTAAGTGTACCTGAAGAGCATGTTAAAAAGTTTAAGTTATCACTT GGAGAGCAGATTCTTGGCCCTGCCCCTTGATCTGTTTGAGGGGTGTGC
stSG4340	76 G A ---	---	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGAGATAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109 A C ---	---	---	TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATAGGCAC AAGTCTTGGAAATTTCCATAAGGGATAAAGTGCATCTTTTGCC/GC/C]CCTTCACAACCTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4361 a	24 T C ---	---	---	TTCCCAACCATTTGAGTGACAGAGCT/G]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAATAGG CACAAGTCTTGGAAATTTCCATAAGGGATAAAGTGCATCTTTTGCCACCTTCACAACCTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4376	73 A G ---	---	---	TTTCACTGCTACTGTTTCGGTGTCTGAGTCTCAAACTCTGCTTTCAGAGTCTTCTCCAAGGGGAG AACAG/G]CTGGAAGTCTGGGCTCTGCAAGAGGCCATCTTCCAAAGCCATTCTTCTCAGCTGC
stSG4381	50 T C ---	---	---	GAAGGCCACAACACTCCATAGCCAGAGATGACAACATACGATTTCTT/C]TCAGTCTTGTAGT ATCCACAGTAGTGATGCTGTCCATGTACAGTGCTGTCCAGAACACCCCATTAATTTCCATGCC
stSG4410	79 A G ---	---	---	ACCAATGGTCTGCTATGTGCATCCGATATTTTGGCCGATCTGAAATAGTCAAGGGCTTAACCAT TCAAACACCCG[G]TGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT

stSG443	65	C T	---			AGCAGATCAGTCCACACTTGTCTCTCTCTCTTTAGGAGAGGCTAGGCAGTGAACACATCA/C/
stSG4430	54	A G	---		---	TJGTATGCAATGAGAAAAATAACCAACTGGTAGGATGGGGAGGGGAGGAGGCAATAGGCAC
a						AAATGGAATCTATCTCTGGCTGTCTCTCAGGTC
stSG4448	99	G A	---		---	ATGCACATTAATGAATGGCCTAACTACTGGGAACCTTATAGTAGTTCTATAAGGT(A/G)ATTAAACATA
						GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATAGGCATCAAGAGGGCCATTTT
						CCTCCCTCCCTTCCCTTCCCTTCCAGTCTTCCATACTGTCCCTCCCTCCCTCCCTCCCTCCCTCCCT
						CGCCTAGCCCTGCCCTCTGGGTCACTGC(G/A)TGGGTTAGGCCCCCAAAAAA
stSG4449	92	T C	---		---	ATTAGCCATTCACTCTGCAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGTATGATGTTTACAAT
						TAACTTTGGACAACCTTAAACCTTA/T/C/JTAGTGACATTGCTGTCTAATAATCAAACTACTTCATCATA
						GGCTGAACATAATTATTAAGAGCAAAAGTTACCCCTCCC
stSG4467	42	C A	---		---	CAGACATGAGGGATGGCCCTGTCTCTCTGGGACAGAGCCCTCA/C/AJAGATGATGTCCATGTTTGTGT
						GAATGAACTCAACACTCTTCAGTTTTTAGAGTCACTTTCTGGTATCGAGCGACCACACCGAGGAG
						CACACCCTGCTCCAGGCTGCTGCCCTCTGCACACAGT
stSG4475	21	A C	---		---	ACATGTCACTTCTGACCAGG(A/C)TATTAATAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGA
						TTAAGAGACACAACCTGGACTTTTGTCTTTCTTTACTGTAGCACCCAGGTTTCATG
						GTAACATCTCTGGGGTGGGGTGAGACAAACA/A/GJATGAACCAATAATTAAATACAATTATACATT
						TCAAGGAGACTTTTAACTAGTTAATGTGAACCGCAGCCATCAATGGTTGTTCAGGAAAAAGGAGGA
stSG4477	32	A G	---		---	TGAAGTCTTGTCTCTGGGCAACGTTTGGCTCATTGCAGTCAGACTTGGC
						TGAACCTCAGAGCTGGTGGGAGCTGCAGGCGAGGGAGGCTGGGGGCGCAGATGAGCGCGGGGA
						CAGCAGGCGTCG(C/J)GCCACGTCCTGGCGTTGGTAGAAGAGGACATAGGCTGCCCTTGGACTCGATCT
stSG4531	79	C T	---		---	GATCTCATTGACAGGGGAGACGCTGTTGTCAATCAA
stSG4550	86	G A	---		---	TGCATTAAGGAATGATACGGCATATTTGGGGGACAGAGAACAAGGCTTGATGAGGACAGAGTCTATTT
b						AAAGAGACAGTGGGCACC(G/A)CAATTGGAGGGGAAGCGGGCAGGGTTTAGAGAAC
stSG4550	85	C G	---		---	TGCATTAAGGAATGATACGGCATATTTGGGGGACAGAGAACAAGGCTTGATGAGGACAGAGTCTATTT
a						AAAGAGACAGTGGGCAC(C/G)GCAATTGGAGGGGAAGCGGGGAGGGTTTAGAGAAC
stSG4590	47	A G	---		---	AATCAGGCACAAGCTCGGAGAGAGCAACAAAGCTCTTCTGCAC/A/GJATGGGAGGAGACAC
						CATTGAAAAGGATCGTTCCTTCTTCATGCAAGCAGGCGCTGGCTCCACAGGCATGGTCTCCTTG
						AATCTGTATCACCCAGGCTGGT(C/J)CAATGTACTAGTAGCTTCCACAGGGATTTTTTATACTATTC
						CTATAAGGTTTTATCATGAATAAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTCACATTTATCT
stSG4623	22	T C	---		---	TAATATCTCTCAAGATGCTCTGGAG
						TAAAAAACAACCCCAACAAAAACACCCAGAGTTTTTGTAGTTTTTATGTTTTTTCAGATTTAAAG
stSG4843	102	A C	---		---	GTATTTCTTTCTAGCTTCTAAATTTTGAGTCAT(A/C)ATCAGAAAGTCTTCCCTACTCCCAAGGTGA
						GAAAGGA

stSG4850 a	38 C T ...	...	GGAACTAAACTGGGAATGGCCGAGGAGGAGGGGCTC/TGTGCACCTTGACGGCCACGTCAGGAG AGCCAGCGGTGCTGTCGGGAGGTTTCCAAGTGCTCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCCC
stSG4879	86 A G ...	...	AACCTCTCC AACTCTGAAGGGGGTGACCTCAACCCAGCCCTTGTCTGTAGGTCCTGCTTTTGCAGAATGGCCTG CCCCTGGAGCTGGAGCAG/A/GCTTGGGTGAGCTCTAGGTGGAGGGTGGTGGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A ...	...	ACTGGACTGGCTGCTTGTGAGCCGGCTGAGCGGGCTGGGACTCGGGCTGACCACTCGCTCTTCAG AGACTGCCCGCGGTGACCACGACTACGCTCTGCC/G/AGTGGGAAAGCAGAGGAGGACC
stSG4896	112 C T ...	...	AAACAAATCAAAACCAATCCACAGCAGTCTATGTACAGGGCCACTCCCTGCTCTGCCATAGAGA GGTTGGGGGCGAGCTGAGGAGTGTGGGGCTGGGCACCTTTCT/C/TACGCCACAGGCCCTGAGG AATTAATTGACTG
stSG4932	22 G A ...	...	ACAGTGCCGATGGTTACACAATG/A/JTTGTAATGTATTTAATCCACCTTACGAATGATTAAATGA TAAATCTTATGTTTATTTTCATCACTACCAAAAGGCTGGGTGCAGGGGTGCTGTTCTGGTCT
stSG4950	24 A G ...	...	TCATGACTCCAGGAAAGGTCTT/GJTCITTAGCTTCTCTCCCTACTTTCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A ...	...	AGATACGGGCAAAACACTGGATGGCTTCCTGACAACTTAAGAGGTCTCCGAGTTATTTCTGGTT GGGAACACTGACCCAGCCCTTATTCCTCAAGGACTAGTCATTGGCAAGGAGGATTTCATGAGCC CC/G/AGTGACACAGATGGGGCCCTGCTCTATATTCAC
stSG4961	91 C T ...	...	GAAGGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAGGAAAGTA/C/TJAGAGAGGGCAATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G ...	...	ACTGGTGCCTCTCAGCAGATTCAGGGGTGTCAGGGCTGGTTACCAACAACTCAGTAGGAGTGCAA GGGCT/A/GJTACCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTTCTCCCTTTTCTTGTGTGC AACCTTG
stSG4997	22 T C ...	...	CAAAGGAGAGTAGGAGCCCAAT/C/JTTTAAATGGTTTCTCTCCCTCATGCTATTTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGAGGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAT
stSG6312	37 C T ...	...	ACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAACAC/C/TJATGCCATGCGGGAAATAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107 G A ...	...	GCTCTGGTCAAGCAAATTCAGGACAGAAAGCAAGGACAGTAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTGTCCAC/G/ATAGTTCAGGCAATTAAGAATAT GCAACCCAGAGAATTTCTGTGAAACATTTTGTCTTTGGCCTGGTGTGGACAGAAAGGGTGGCCAA ATGGATTGATGATGAGCAGACATG





stSG8145	97	CT	---	TTGTGGACTTCAAATCTTTCTCCTCAGATTTTAAATGACATTATGCATGTACATATTTTAAATTT AGACACATTTAGAGAACAAATTTGTGAA[C/T]ACAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATCAAACACTTATCTTAACTGACTCTGTCAATCTCTGCTGTGAAGG	
stSG8150	36	A	G	---	ATTGTTCTTGCAATTGCTTGGATTTTTCAGAATAGTGA/GATATAATAAATACGGGAATCCTAGGCAT TCGTGTTTTCTATGTTTTTAACAGGATTTTCTCTAATGTTTCGCTATTAAATACCATGCAGGAAATT GGGAAAT
stSG8340	30	CT	---	---	AGAGGATTATGGAGAGAGCTGGGCAGGATC/TCAACATTATGACCCCTGAACCTCCAGAACCTGGAT TCACTAGAAGGAGAGAGAAAAACGCTCATCAAAA
stSG8466	111	G	A	---	TGTGTTATGGGTGACTGTAGCCTAAGGATAAATGAAATAAATGACAGCAATGTTATAAGCAGTGGGA GGAGTGAACCTGGGAATACTTGGTTACAAGGTATTTGCACACTACCT[G/A]TGAAGACGACACAGCATTAT TTGAAAG
ESTD-ACE	--	--	--	---	GATCAAGCAGTGCACACGGGTACGATGGACCAGCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCCCTCTCCTCGTCGGGGGCCAACCCCGCTTCCATGA GGCCATTGGGACGTCTGGCGCTCTCGGTCTCCTGAACTCTGCACAAAATCGGCTGC
ESTD-ADA	--	--	--	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGCCCTGGGGAATCCAGGGTCACTGTTCTCTCTGCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAACTGGGACTGTGAGGACATGGAGCCCTCGGCACTGAGCTGCAGACCC GCAGACAACTCCTGAGCTTTCTGGGCCTCTGAGTCTTGCTCTC
ESTD-AK-168	--	--	--	---	GGGAGTGACAGCTAGAGCACCAAGGGGGCTCTACAGCTGTGTTCTCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	--	--	--	---	AATCCCAGCACCTTTAGGAGGCTGAGCGGCATATCACAGAGGTGAGGATTTGAGACCAGTCTGA CCAAATGGTGAAACCCCATCTCTACTAAATAACAAAATTAGCCAGGCATGGTGGTGCATGCCTGT AATCCCAGGAGGCTGAGCAGGAGAAATCGCTTGAACCTGGGAGGCGAAGTTGTGGTGAGCCGAGAT GGCAOCATTGCACCTCCAGCCTGGGCAACAAGAGTAAACTCTGCTCTC
ESTD-ANT1	--	--	--	---	TCTCCTGTGCTATTCCTACTCCATTAGTTCAAGGTGAGTGAAGAAGTGGGCAATTAAACCAAGTAATTCA TGGACTGCCCAACTCGAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD-APOA2	--	--	--	---	CCAGGTGTTGTGGCAGTGCCTGTAATCCCAGCTACTCGGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGGAGCGGAGGTTGCAGTGAGCTGACATCGCGCCACTGCACCTCAGCCTAGGTGACAGAGCAAG ACTCC
ESTD-ARSB	--	--	--	---	GGAAGAAATGGAGCCTGTGGGAAGGAGCGCTCCGAGGGGTGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAAGGCGTGAAGAACCAGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGAGTGTGGAAACCACATCAGTGAA GGAAGCCCATCCCCAGAAATTGAGCTGCTGCATAATATTGACCCCAAC

[illegible]

ESTD-C7	--	--	--	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	--	--	---	---	GGCAAGTTTTATTGATAGAGAGGAATCAAATAATGGCAATGAGGAGACATACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGGCAGTGCCAACCCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGTAGAACCATCAAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCTAG TAACATAATTGTGCTTCATTATGGTCTTTCCCGGCCTTCTCTCACACAG
	--	--	--	---	---	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCTTTCCCGGCCTTCTCTCACACATACACAGAGCCCTACAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTTCCAGAGACCTGAAAAACGTGTTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD-CB23	--	--	--	---	---	ACCAGGACAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGTGGCTGTGTTTGAGCCATCAGAGCAGAGATCTCCACACCCAAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCGACACGCTGAGCTGGTGGGTGAATGG GAAGGAGTGCACAGTGGGGTACGACAGACCCGAGCCCTCAAGGAG
	--	--	--	---	---	GTTTCTTTCAGACTGTGGCTTCACTCCGGTAAGTGAGTCTCTCTTTTCTCTCTATCTTTCGCCGTG TCTGCTCTGAAACCGGCGATGGAGATCCACGGACACAGGGCGTGAGGGAGGCGCAGAGCCACCTG TGCACAGGTACCTACATGCTCTGTTCTTGTAACAGAGTCTTACCAGCAAGGGTCTGTCTGTGCCACC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCGGTG
ESTD-CB25	--	--	--	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTAGCAATAGGCTAAACCAATAAAAAAT TGTGTGTGGGCCTGGTTGCAATTCAGGAGTGTCTGTGGAGTCTGCTCATCACTGACCTATCTTCTGA TTTAGGGAAGCAGCAATCCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAAATGCTGCT TTCTCTGTTTCATCTGATGGAAAGTCTCAACACCAATTTCCATAACC
	--	--	--	---	---	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTCCCTGTCACTTTCAGGGTGTCAAGGTGGAAGGT GAACAGGGTCCCGTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCGCTTTG GTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD-COL2A1c	--	--	--	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTGCTGGACCTGGAACACTGGACTCTTCTACTGAGAGACAAGACTTACCC AAGAGAGATTAAATGGCAAGATATACAATAACAATTTTATTGACCAAAACACTATCATGGAACAGC ATT
	--	--	--	---	---	GCCGCAATGCCGGGAGTTTCTCCAATGTGTGGAGAAGCCCTTAGAAGACATGTTTGATGCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGAGATGAAAGCTACCATCTCCTCATCATGAAAAC TGGGAGGCCGGCATAGTCTCATGCTGTAAATCCAGCATTTTGAAGGCTGAGGGGGTGGATCAG TTGAGGTCAGGAGTTTGAGACCAACCTGGCCAAACAT
ESTD-COL2A1d	--	--	--	---	---	
ESTD-CPT2	--	--	--	---	---	

ESTD- CTLA-4	--	--	--	---	---	ATGGCTTGCTTGGATTTACAGGGGACAAAGGCTCAGCTGAACCTGGCTACAGGACCTGGCCCTGCAC TCTCCTGTTTTTCTTCTTTCATCCCTGCTTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCAAAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	CAGGCCAGCGTGGTCGAGGTGTCACCATCCGCGCAGAGAACAGGTCAGCCACCATATGCACAGGT TCTCATATTGAAGCTGCTCAGGGTTCCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	AAAAAACATTTTAACACCTTTTCAATCATATACACCATAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTTCCAAATTACTTGAATCTAAATGTACATACTGATTAAATGCAAGTTCAACAGACA ACTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCCATAT CTGCAATGTC
ESTD- D17S33	--	--	--	---	---	CATCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGCGCCCTACCCCTTTGTAGTCCATGGGAAGGCTCCTCTGGGGGGTG GGGTTGTGTGGCTATGTGTGGTCTTGTGTAGACGGGGGCTTTGGTTTCAGTTGCACATTTGGGTTATT GCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	TTTGAGACCACCCCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATTTACAAAATTAGCTGGGTGT GGTGGTACATGCCTATCGTAATCCAGCTACATCGGGAGGCTGAGCGAGGAAATGCTTGAACCCA GGAGGCAGAGCTTCAGTGAGCCAAAGATCACACCTGCACCTTACAGCCTGGGTGACACAGTGGAGA CTCTGCTCTCAA
ESTD- D3S11	--	--	--	---	---	AACTGATTAGAACCTGAAATACATATTTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTTAAAAATCCAATAAAGTACACGTAAATAAGAAATTTAACAGAAATATCATTTGT TTATTCAAACTATTTATCACCTTATTTTATTTGGTAAGCCATACATAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCAGGAGCCTTGATGTCATTTCTGTATCTCCTCAG GTATCCACCTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTTGTTATTAAATTCAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAATATGGTCAGTTACAGCTGATTTCCC AGAAGTGAACATACTGCTCCTAGAACCCAGAGTCATCTGGATGTTCTGTTCCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTTGGAAAGGATGCCGGTATGT
ESTD- D4S338	--	--	--	---	---	TTTTCTGTTTACCTTGTTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAATGTATTT CTTAAACAATAAAGTTGAAAGTCCAAAATTAATCCTTGATCCATGGACTGCAGAAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGCATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGTATT GCCAATAAGCAGTAATATTTGAGAGGAATCTGTTTTCATGCAAGTAG
ESTD- D4S95	--	--	--	---	---	CTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAAATTTTGAGAAAGAGCAAAACAACTTTCAAGG ATAATGGGGCAATCACITTTCTTTCTTTTAGAGTCTACCGG

ESTD-D7S399	..	--	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCTTTTACAAACATTTTCATCCATGGACTCCATAGT AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	--	--	---	---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGGCTGGACCTCACTGTCCTGGGAGAGAGAGGGAGTGGGGAGGGAGACA GAATGCTGATTATCTGGTGAGAACCAAGAACTTCTGGCCTGTGGGTAGGGGAGCTGCTTCCAAGACG TCCTGATTTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD-DRD1	--	--	---	---	---	TCCCAGCCTATCGGTCTATTTGGACTATGACACTGACGTCTCTCTGGAGAAGATOCAACCCATCAG ACAAACGGTCAGCACCCCAACCTGAACCTGCAGATGAATCCTGCCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTGCTATTAGAAACTAAGGTAC
ESTD-DRD2	--	--	---	---	---	TCTGCCTTTGGTGAGGAGGCTGCCGGCGAGCCAGGAGCTGGAGATGGAGTGTCTCTCCAGCACCA GCCACCCGAGAGACCGGTACAGCCCCATCCACCCAGCCACCAAGCTGACTCTCCCCGACCCG TCCCACACGGTCTCCACAGCACTCCCGACAGCCCCGCCAACACAGAGAAGATGGGCATGCGAAAG ACCAACCCAAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCAATG
ESTD-DRD3	--	--	---	---	---	AAGCATGGCCAGGATGAGCGCGAGTAGGAGAGGGCATAGTAGGCATGTGGGGGGGCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTTCAAGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGTGGGTGATGCCAAGGGGCTTCTGTGAGGAGA
ESTD-ERB2	--	--	---	---	---	TCTTCAGGATCCGCATCTCGCCTGTGGTGGGCATCGCTCCGCTAGGTGTCAAGCGCTCCACAGCTGG GGTGAGGGGTGGTGGGTGAGTGGCGGGGGCGGTGCAGACCCACGCGGCTGGGAGGACTTCAACC CGCCTCACTCCGTTTCTCTGCAGCAGTCTCCGCTCGTGTACT
ESTD-ETS2	--	--	---	---	---	ACTCACAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGGCCACCAAGAGCCGCTCTGGCGCCTGGCA GTCCGTGGGACGGGATGGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGTGCTGGACACACAC AGACTATTTTAGATTTCTTTTGGCTTTTGAACCAAGGACAGCAAAATGCAAAAACCTCTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCTATTCAGAAGTTAGTTTG
ESTD-F2	--	--	---	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCCTCCAGGCCGTAGGGGAACTGGGGGATCTAGGGGATGGGTAGGAAATGGCCC AGCCAGTCCCGGCGGTGCTGGTGGTCCAAACAGAGAGGCGGTGGAGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	---	---	---	AGATCCTGATGATTTTTTCTTATTTTTCTAAATGTTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTTGAAGTAAATTTGTAAAGTATGATGTTTAACTCAAACTTCATTTTTTTTTTCCATA GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC



ESTD- IGHV4-6	--	--	--	--	---	---	---	TTTACTATTTCAATGGATACAGAAATTGTGGGAGTCACTATATTCCTATGAACAAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCCTACATTGTGTAGTGAACGGGAGTGGTGGATCCGAGAGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACCTGAAAGT ATGTAATACTTCACAAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	--	--	---	---	---	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATATTATTATTATTATTTATTTT AGATGGAGTCTGGCTGTGTACCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCTCTGGGTTTCATGCCAATCTCTGCTCAGCCTCCGAGTAGCTCCGAGTACAGGACACCCGCCACT GTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCAACCGT
ESTD-IL1B	--	--	--	--	---	---	---	CCACTACAGATGGATAAATGGGTACAATGAAGGGCCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTCTCTGCTCAGGAGCTCTGTGCAATTGCAGG
ESTD- KRT10	--	--	--	--	---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCATACTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCATTTGATA
ESTD- KRT8	--	--	--	--	---	---	---	ACCTCACCCCTCCCTTAGCCGTGGGAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAAAGCAGGGCCTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCACGTCAACATTGACACA
ESTD- LF79	--	--	--	--	---	---	---	GGGTGATTTGAGGCTCAGTTAATTTCAAAATTTAACCCTAGCAAAACGCAATGGTATTGATA AAAAATAAAATTTCCAATATGATGTGCTGTATTACCTGCCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCAAGAGGGCTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	--	---	---	---	TACACACTTTCCTTACCCTTCACTGAAACGACTCGCAACTGGAGCCTGTAGGAATGGAGTTGA CCTTCCCAAAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	--	--	--	--	---	---	---	TGTCAGTGTCCCTAGGGCACTCACCACCTCCAGCTTCTTCAGCTCTGGCCTGTCTGCTGCCTGCA AGGTTTTGCTTAATCTCAATTCATGCTCTTCATCTTTTAGCAGCTGTGGGTTTTGTTGTTTC TTCGTTTTTGCTTAGTATCTGACTACTTTTTTAATATAAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTATTAAAAATTTTTCACCTG
ESTD-MCC	--	--	--	--	---	---	---	TTGTCAGGAGTGTGCTGATGCTGCCCTCCCAAGCTCTGCCCTAGCCGAACCTCAGGACAACTGCAG CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGAA TCTCAGGAAGTCTCTGCTTTCCAAGGGTTTGGTCTAAGTTGCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATGTGTTCTCTGTTTAGCATGG
ESTD-NF1	--	--	--	--	---	---	---	ATTATCCAGATGAATTTACAAAACTATACCAGATCCACAGACTGATATGGCTGGT





ESTD-RDS	--	--	--	---	---	---	CCCGAGGAATCTGAGAGCGAGAGCGGTGGCTGGCTGGAGAGAGCGGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAGCTGGCAAGGCAAGGCAACAGGTGAAGCCGAGGCGCGCAGACGAGG CCAGGCCCAAGAGGCTGGCTGAGGCGCTGGGGCCCTCCCTCCGAACTGAGAAATAGTGCACCT CCAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- RYR1	--	--	--	---	---	---	CTTCGTACGGGAGGTACGCTCCGCTCTTCATGGACATATGGATGAGTGTCTGACCAATTTCCC CTGCTGACAGTATGACCGGAGACTTGTCTACTATGAGAGGGAGCTGTGTGCACTCATGCCCGC TCCCTGAGGCTGGAGCCACTGAGAATCAGCTGGAGTGGAGCCACCTGCGCTGGGGCCAGCCACT CCGAGTCGGCATGTCACTACCGGGAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	---	---	---	TGAACACCCCTGTGGTCCGGAGCCAGGTGTGTTCTCTGGAGCCCTGAGGAGTTGTGTCTGTGTG CAGTCCCCCGGCCACCTGCTGGTTGAGCCTGGACATACACCTTCACCTCTTTGGCCCGGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCTGTGTGACACCCCTCTGTGAAGACCCCAACCCCTGCCTCC CCACCCAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	---	---	---	TTACATTTGTGGATTGTTCTTTGTGTGCGAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGCTGTGCTGTGGGATATTTGAAGAGATCTTTGCCAGTCCAATGTCTCTAGAGAG TTTTCCCAATGTTTCTGTAAATAGTTTCATAGTTGAGGCCCTAGATTAAAGTCTTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	--	--	--	---	---	---	AAATGGTCAGGACCCCTGATCCACAAGAAGTGTGTTACCATTTTCATCAGGGCCATCAGTTTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTTGTGGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTTTACAACCTTTCTCCAGTATGGATGGGATTATGATGGGGG GAGAAGCAAAATTTTAAATAGGACCCCATGAGACACATCA
ESTD- THRB	--	--	--	---	---	---	TGCGGCTTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTGATTTCCAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCCGAGTCTCAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAACAGACCACAGACCTGTGTCCTCCAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCCAGAAGACCCCTCAGAATCGGAGCAGGGAGATGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCTCAACTTTCCAAATCCCGCCCGCGGATGG
ESTD-TYR	--	--	--	---	---	---	TAGTGAAGTTTTCATCTCTGTGAGCTTCTGGATTCTTGTCCACCGCAACAAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCAATAATTTGATGTGCTGTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGTCCCTATGGGATGACA

[illegible]

EST11458 6	..	--	--	---	---	CCACTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCCTCCAGTGCTCATCTTGTTCTCGAGTTTT CTCTGCCATGTTGCTATTGACGACGGACCTGTCCCAAGCCAGATGATTTACCATTTCCACAGTGGT CCATTAAACAATTCTATGAGCCAGGAGAGATACGTATTCCTGCAAGCCGGCTATGTGTCC CGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	--	---	---	CGGCTTCCTCCAGGTATTGTCAGAAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTAGTACACCTTCCCACTCTCTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAAGGCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	--	---	---	ACCTGGTGTGCTGGTGTGCTGGTGAACCTGTGCTCTTGCAATTGCGGCCCTCTGCGGCCCTGG TCTCTGCTGCTGGGTAGTCTGGAGTCAACGTGCTCTAGTGAAGCTGGTGTGATGGCAACC CTGGGAACGATGGTCCCAAGGTGCGATGTTCAACCCGACACAAAGGAGAGCGGGTTACCCCTGG CAATAT
EST36027 2	--	--	--	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCCTGCAAGAACAGCATTCATACATGGATGAGGAGACTGGAAACCTGAAAAAGG CTGTCACTACAGGGCTTAATGATGTTGAACCTGTTGCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTGTAGATGGTCTCTAAAAGACAAATGAATGGGGAAGACAA
EST12274 0	--	--	--	---	---	CCCCAGTTGACAGCCACTGCTAGACTAAGTTCTTGCTTCCAATAGAGCCTTACCAAAGTGAT TACATAAAGAAAGTCAAGTGTTTACTCCTCATGACCAATATCTTCCCTCCTTAGGATGAGGTGA TAGTAAATGACCGATGGGTGAGAACTGTTCTGTCAACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 EST44438 7	--	--	--	---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCTGTAGCCGATTGTCTATCTCCAGCGGCCCTGTCTATC CAGCTCACTCATCAATGGGCCAGTCAAGCCAGGCACTGGGCTCCGGAGGACTCAACCACTGCCCT GCTGCCATGTGGACTGGTCAAGTTGAGGACTTCTTG GCAGCCAGGAGCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCCT GCTCCGACCTAAGCGGAGCAGCTCAAGAGCCGAGCGGAGGTGGG
EST12839 3	--	--	--	---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACCTTGAATGTTATTCAACTGG ATTTCCAGTAGTTTCAGTTACTTATGAATATATGATACCTTAGCTTAG
EST54419 8	--	--	--	---	---	CTTCTGCCATTTGAATGATATTGTTGCTGTGGACCTGAGCATTATGGCAAAATGATCACTA TTTTCTGACCCCTACTACAATCCTGGGAGATGATTTGGGTTAGCGTGGTGTGTTGTGTCTACTA TAGTCCAAAGTGAA

EST10398 2	--	--	--	---	---	---	TGCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTTACATTTGGGGCTTGACITTTCAACACGAGGAAG CATTGTTTCTTCGGGCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTG
EST36751 7	--	--	--	---	---	---	CCAAAGTGTTCAATTTTAGCTTGCAGGTTTAACTCGATTACTTTTCTATTCAAACTCTCTGTAAAA TTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	--	--	--	---	---	---	CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTCTGCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCAATTAAACAAATATTTTACCTTTTGAATAAATAATG AAGGATTTGACCTGCTTGGCTCTGGAAGAGATATCCGTACCGTCTGACGTTTGAACAATACAGAT GCCTTCCCTTGTAGCAGTTTTCAGCCTCTCTACCCCTA
EST18288 3	--	--	--	---	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCAACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTATGACAGGCTGTACAGGATGGAAGACTGGCTGCTCCCTGACGGGAGCCAGTGTGG ACAGACCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAAGGCAAACTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	--	---	---	---	TTCCGGCAGCCCCCATCTTGGACCTTGGTCCCTCGTCCCTCAGGGGCCACCCCGCGGCACTCACCGCTCT CGCTCTGGTAACATCCGGCGGGCGGCTCTTGGACACATAGCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTCTGTCGGGGCTTGCAGGGGCCAGCCCTGCAGAGAGAGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
EST58707 7	--	--	--	---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATACCTTATCATCAATTTGTTACAGGAGGCTTT AAGTTCAGGATCTTGGCTACATGAAGGCCAAATTCGAGAGACCTTAGAATACACGAGACCGA ATGTATCAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATAGCA CACTTGTCACTACATTTCTGATTGGTGGACTCTTGTCTAAGAACCTT
EST74167 6	--	--	--	---	---	---	AGACCATGAAGGAGTTGAAGGCCTACAAATCGAACTGGAGGAACAACCTGACCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGGAGCTGCAGGCGCGCAGGCGCGGCTGGCGGACATGGAGGA CGTGGCGGCGCGCTGGTGCAGTACCGGGGAGGTGCAGGCGCATCTCGGCGAGCAACCGAGGAGC TGCGGGTGGCGCTGGCTCCACCTGCGCAAGCTGGTAAAGCGGCTCTC
EST43211 8	--	--	--	---	---	---	CGCTGTGTCAGTAACCGGGGAGGTGCAGGCGCATGCTCGGCCAGACCGAGGAGCTGCGGGTGCG CCTCGCTCCCACTGCGCAAGCTGCGTAAGCGGCTCTCCCGATGCCGATGAOCTGCAGAAAGCGCC TGACAGTGTACAGGCGGGGCGGAGGGGCGGAGGCGGCTCAGCGGCATCCGCGAGCGGCTG GGGCGCTGTGTGGAACAGGGCGCGGTGCGGGGCGGCGGCTGTGGGCTC
EST36770 4	--	--	--	---	---	---	TGTAGCCAAAGTCACCTGCATCATCATTTTGGCTGTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCATTATGATGCCAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATACTGGGTTCTGTTCTCTTCTGATCAT TCTTACAAGTTATACITCTATTGGGAAGGCCCTAAAGAAGGCTTAG

EST26021 1	--	--	--	---	---	TAATGTAAGCTCATCCACCAAGAGCCTGCACCATTGTTTGGAGTTGAGTGACATGTTGCGAAACCTGT CCATAAAGTAATTTGTGAAAGAGGAGCAAGAGAAACATTCTCTGCAGCACTTCACTACCAAATGA GCATTAGCTACTTTTCAGAAATGAAGGAGAAATGCAATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTTTTGCACAAAGACAAAGCAAGCCC
EST51212 0	--	--	--	---	---	ATCTGAGCTCGCCAATAAGCTTCTTGGTTCTACTTCTCTCCACAAGCCCCAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATAACAAAAGGCGCCTCTCT ACATCT
EST20118 2	--	--	--	---	---	GTCCGAATCTCTCTGAAAGTGCCCGGTTTAACTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGGCTTGAAGCTGGGAGTGGGTTTAGGACGCGGTTCTGCGTGCATCCTAAGCTCT GAGAGCAAACTCTCTTGAAGCTGGGAGTGGGTTTAGGACGCGGTTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	--	--	--	---	---	ACAATCAGGTCACACATTCCAGAAGAGGAGGGTGTGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	--	---	---	CTTCTATGGGATTGACTTTATTTCTCCATTGTCTTACCTTTACAGGTGTTAATATAGTGAAGG GAAGCTGCAGCTCATGACAAATTTGAAGCTGACAAATTACACAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAACCTGGTGTACCTTTAATACAACCTAG CAGACGGAAGTGAAGTCAAGGTAAGAAAT
EST34088 2	--	--	--	---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGGTATAAAGGGGCCACACAAGAGACCGGCTCAAGG ATCCCAAGGCCCAACTCCCGAACCACTCAGGGTCTCTGTGGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	--	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCAACCCCTCTTTCTCTCCCTTGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCCAGCAAGAGAAAGAGAACCCAGAAAT CACAGGTGGCACGTGCGGTCTACCGCCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
EST74082 0	--	--	--	---	---	TCCAGGTGGCTGGACCCAGGCCCCAGCTCTGCAGCAGGAGGAAGTGGCTGGGCTCGTGAAGCATG TGGGGTGAGCCAGGGGGCCCAAGGCAGGGCACTGGCTTCAGCTGCTCAGCCCTGCTGCTGCTGCTG CCAGTCACTGTCTTCTGCCATGGCCGTGTGGATGCGCCTCTGCCCCCTGCTGGGCTGCTGGCCCTC TGGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGCG
EST45311 0	--	--	--	---	---	GCCCTCCTCTCTTCCAAATCTGTCCCTATAGTTTTCTCTATTAAGTGAACATACATGCTTTTAGT GGATAGATGCACAAACACACAGCCATTATGGGAAGGATCCACGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTTCATTTAACAGCCCTTATTCATGCGCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTTGTGAAT



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## EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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## CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,  
or a portion thereof which includes a polymorphic site,  
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is  
biallelic.
8. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is the reference base  
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is an alternative form  
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a  
20 segment of a fragment shown in the Table, column 7 or  
its complement.
11. The allele-specific oligonucleotide of claim 10 that is  
a probe.



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12. The allele-specific oligonucleotide of claim 10,  
wherein a central position of the probe aligns with the  
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is  
5 a primer.
14. The allele-specific oligonucleotide of claim 13,  
wherein the 3' end of the primer aligns with the  
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which  
10 is selected from the group consisting of the nucleotide  
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which  
is selected from the group consisting of the nucleotide  
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the  
Table, column 7 or the complement thereof, wherein the  
polymorphic site within the sequence or complement is  
occupied by a base other than the reference base shown  
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising  
obtaining the nucleic acid from an individual; and  
determining a base occupying any one of the polymorphic  
sites shown in the Table.
19. The method of claim 18, wherein the determining  
25 comprises determining a set of bases occupying a set of  
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
- 5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.